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Thu Dec 29 08:14:05 2005

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CAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVEIAYHP 240
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                                                                                                                                                                                                                                  | Sequence 46. Application US/09660587
| Sequence 46. Application US/09660587
| Patent NO. 6392023
| GENERAL INFORMATION:
| APPLICANT: Walker, David H.
| APPLICANT: Walker, David H.
| APPLICANT: Yu, Xue-Jie
| TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
| TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
| TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
| TITLE OF INVENTION UNMBER: US/09/660,587
| CURRENT APPLICATION NUMBER: 09/261,358
| PRIOR PILING DATE: 199-03-03
| NUMBER OF SEQ ID NOS: 46
| SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ITKKIFALGLDKSBINTHSNFTRSYDPTYASSFAGFSGIIGYYVNDFRVEFEGSYENFEP
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100.0%; Pred. No. 2.3e-147;
iive 0; Mismatches 0;
US-10-314-639-58
US-10-059-964A-58
US-10-314-639-18
US-10-314-639-18
US-10-059-964A-18
US-09-60-587-40
US-09-811-007A-40
US-09-314-701-32
US-10-314-639-32
US-10-314-639-32
US-10-314-639-32
US-10-314-639-32
US-10-314-639-32
US-10-314-639-50
US-10-314-639-50
US-09-314-701-44
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Best Local Similarity 100.
Matches 271; Conservative
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): /cgn2_6/ptodata1/iaa/H_COMB.pep:*
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): /cgn2_6/ptodata1/iaa/PGTUS_COMB.pep:*
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-019-964A-48
US-09-201-314-639-48
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US-09-201-458-6
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US-10-059-964A-4
US-10-059-964A-3
US-10-059-964A-3
US-10-059-964A-3
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US-09-314-701-24
US-10-059-964A-26
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seq length: 200000000
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Sequence 48, Application US/09314701
Patent No. 6544517
GENERAL INFORMATION:
APPLICANT: Rikihies Yasuko
APPLICANT: Rikihies Yasuko
APPLICANT: ODASI, No. 6544517io
TITLE OF INVENTION: Chaffeensis
FILE OF INVENTION: Chaffeensis
FILE REPERENCE: 22727/04021
CURRENT APPLICATION NUMBER: US/09/314,701
CURRENT PILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 48
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                                                                                                                                                                                                                                           109 VEFEGSYENFEPER--OWYPENSOSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVC 166
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                           50; Mismatches
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Best Local Similarity 40.5%;
Matches 115; Conservative 5:
      40.5%;
  Best Local Similarity 40.5
Matches 115; Conservative
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US-09-811-007A-42
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Patent No. 6392023

GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2
CURRENT APPLICATION NUMBER: US/09/660,587
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION UNMBER: 09/261,358
PRIOR APPLICATION UNMBER: 09/261,358
                                                                               APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
APPLICANT: Walker, Jere W.
APPLICANT: William Street W.
APPLICANT: Yu, Kue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2
CURRENT APPLICATION NUMBER: U8/09/811,007A
CURRENT FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-09-12
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                    Sequence 46, Application US/09811007A Patent No. 6660269 GENERAL INFORMATION:
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SEQ ID NO 46
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SEQ ID NO 42
LENGTH: 280
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US-10-059-964A-48
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US-10-059-964A-48
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US-09-660-587-10
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Patent No. 6893640
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE CANTER RIAINER, Yasuko
TITLE OF INVENTION: Chaffeensis
TITLE OF INVENTION OWNER: US/10/314,639
CURRENT APPLICATION NUMBER: US/10/314,701
PRIOR APPLICATION NUMBER: US/09/314,701
PRIOR APPLICATION NUMBER: US/09/314,701
NUMBER OF SEQ ID NOS: 66
SOOTH NO. 40 CONTROL OF TOWN OF TOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEFEGSYENFEPER -- OWYPENSQSYKFFALSRNATHSDNKFIVLENNGVVDKSLNVNVC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 IELEAAYQQFNPKNTDNNDTDNGEYYKHFALSRKDAMEDQQYVVLKNDGITFMSLMVNTC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHK 225
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                APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
APPLICANT: Walker, Jere W.
APPLICANT: McBride, Jere W.
APPLICANT: Wix Vue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REPRENCE: D6152CTP2
CURRENT APPLICATION NUMBER: US/09/811,007A
PRIOR APPLICATION NUMBER: 09/660,587
PRIOR APPLICATION NUMBER: 09/660,587
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein US-09-811-007A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 509.5; DB 2; Pred. No. 7.5e-47; 50; Mismatches 98
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Similarity 40.5%;
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Matches 1151 Conservative
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US-10-314-639-48
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GENERAL INFORMATION:
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US-10-314-639-48
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LENGTH: 280
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APPLICANT: OHASHI, NORIO
TITLE OF INVENTION: OTTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA
TITLE OF INVENTION: CHAFFEENSIS
FILE REPERBYCE: 22727-04109
CURRENT APPLICATION NUMBER: US/10/059,964A
CURRENT FILING DATE: 1099-05-19
PRIOR PILING DATE: 1999-05-19
PRIOR PILING DATE: 1999-09-18
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 YDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHK 225
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                                                                                                                                                               YDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHK 225
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1 MNYKKILVRSALISLMSILPYQSFADPVGSRTNDNKEGFYISAKYNPSISHFRKFSAEET 60
                                                                       1 MNYKRFVVGVTLSTFVFFLSDGAFSD---ANFSEGRRGLYIGSQYKVGIPNFSNFSAEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48, Application US/10059964A
; Patent No. 6923963
; BENERAL INFORMATION:
; APPLICANT: RIKIHISA, YASUKO
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RESULT 10
US-09-201-458-6
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APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-Jie
JITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2
CURRENT APPLICATION NUMBER: US/09/660,587
CURRENT PILING DATE: 2000-09-12
PRIOR FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 10
LENGTH: 283
LYPE: PDFT
TYPE: PDFT
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Patent No. 6403780

GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
APPLICANT: Walker, Jere W.
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP
CURRENT APPLICATION NUMBER: US/09/261,358A
CURRENT PILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1998-11-30
PRIOR FILING DATE: 399-01-03
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35.4%; Score 507; DB 2; Length 283;
Best Local Similarity 40.3%; Pred. No. 1.4e-46;
Matches 116; Conservative 46; Mismatches 100; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
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ORGANISM: Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-261-358A-10
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LENGTH: 283
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1 MNYKRFVVGVTLSTFVFFLSDGAF-----SDANFSEGRRGLYIGSQYKVGIPNFSNFSA

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61 EEAPINGNTSITKKVFGLKKO-GDIAQSANFNRT-DPALEFQNNLISGFSGSIGYAMDGP 118
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                                                                                                                                                                        108 RVEFEGSYENFEPERQWYPENSQS-----YKFFALSRNATNSDNKFIVLENNGVVDKSLN 162
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                                                                                                                                                                                                                                                                                                                        234
163 VNVCYDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09201458A
Patent No. 6458942
GENERAL INFORMATION:
APPLICANT: Walker 1
APPLICANT: Walker 4
APPLICANT: W. Xue-Jie
TITLE OF INVENTION: 28-kDa Immunoreactive Protein Gene of Ehrlichia
TITLE OF INVENTION: canis and Uses Thereof
FILE REFERENCE: D6152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1B
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                                                                                                                                                                                                                                                                                                                                                                                                  35.4%; Score 507; DB 2; Length 283; 40.3%; Pred. No. 1.4e-46; ive 46; Mismatches 100; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/201,458A CURRENT FILING DATE: 1998-11-30 NUMBER OF SEQ ID NOS: 21 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-09-314-701-4
; Sequence 4, Application US/09314701
; Patent No. 6544517
; RENERAL INFORMATION:
; APPLICANT: Rikihisa, Yasuko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Ehrlichia chaffeensis
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Matches 116; Conservative
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APPLICANT: OHASHI, NORIO
TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA
TITLE OF INVENTION: CHAFFEENSIS
FILE REFERENCE: 22727-04109
CURRENT APPLICATION NUMBER: US/10/059,964A
                                                                                                                                                                                                                                                                                                                              APPLICANT: CARSIS, No. 6893640io
TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
TITLE OF INVENTION: Chaffeensis
FILE REPERRICE: 22727/04021
CURRENT APPLICATION NUMBER: US/10/314,639
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US/99/314,701
PRIOR APPLICATION NUMBER: US/99/314,701
RIOR PILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1283
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                             RVEFEGSYENFEPERQWYPENSQS-----YKFFALSRNATNSDNKFIVLENNGVVDKSLN 162
                                                                                                            61 EEAPINGNTSITKKVFGLKKD-GDIAQSANFNRT-DPALEFQNNLISGFSGSIGYAMDGP 118
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                                                                                                                                                                                                                                                                   ; Sequence 4, Application US/10314639
; Patent No. 6893640
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APPLICANT: RIKIHISA, YASUKO
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local Similarity 40.3
Matches 116; Conservative
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US-10-059-964A-4
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US-10-314-639-4
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              TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia TITLE OF INVENTION: Chaffeensis FILLE REFERENCE: 2272//4012 CURRENT APPLICATION NUMBER: US/09/314,701 CURRENT FILING DATE: 1999-05-19 NUMBER OF SEQ ID NOS: 66 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 EET-1PG---ITKKIPALGLDKSEINTHSNFTRSYDPTYA---SSFAGFSGIIGYYVNDF 107
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35.4%; Score 507; DB 2; Length 283
Best Local Similarity 40.3%; Pred. No. 1.4e-46;
Matches 116; Conservative 46; Mismatches 100; Indels
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US-09-314-701-4
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Sequence 30, Application US/09314701

Sequence 30, Application US/09314701

Sequence 30, Application US/09314701

SERNEAL INFORMATION:

APPLICANT: Rikihisa, Yasuko

APPLICANT: Rikihisa, Yasuko

TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia

TITLE OF INVENTION: Chaffeensis

FILE REFERENCE: 22727/04021

CURRENT APPLICATION NUMBER: US/09/314,701

CURRENT PILING DATE: 199-05-19

NUMBER OF SEQ ID NOS: 66

SOCTRANARE: PALENTI Ver. 2.0
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CURRENT FILING DATE: 2002-01-28
PRIOR APPLICATION NUMBER: 09/314,701
PRIOR PLING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/100,843
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 4
LENGTH: 283
                                                                                                                                                                                                               ORGANISM: Ehrlichia chaffeensis
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Search completed: December 28, 2005, 15:43:04 Job time : 31 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 28, 2005, 15:02:01 ; Search time 111 Seconds (without alignments) 1722.506 Million cell updates/sec Run on:

US-10-731-554-46 1434 1 MNYKRFVVGVTLSTFVFFLS......ASATLNTDYFGWEIGFRFAL 271 Title: Perfect score: Sequence:

2166443 segs, 705528306 residues Searched: Total number of hits satisfying chosen parameters:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

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SUMMARIES		171 EHRCA	V2 EHRCA	.97 EHRCH	306_EHRRG	B8 EHRRU	X5 EHRRU	1 1	1	Y1 EHRRU						3L4 EHRRG	CD9_EHRRW	3D6_EHRCH	176_EHRCA		358 EHRCH	TU1_EHRCA	1 1	CU2 EHRCH	5Y9 EHRCH	Q4W4X0 EHRRU	3M2_EHRRG	C7 EHRRU	QSHA16_EHRRW	SY7 EHRCH	1 1	CY4_EHRRU
03	Ω.	Q9F471	Q9ADV2	069197	Q5FGQ6	Q4L0B8	Q6VCX5	Q5HA08	Q4M4M3	Q5W5Y1	Q5HA10	Q9WW41	Q9R443	086812	Q4L0C0	Q5FGL4	Q5FCD9	<b>08G8D6</b>	Q9F476	88	085358	0841	09L	Q9ACJ2	Q9L6Y9	Q4W	O5 FGM2	04L0C7	O5H2	Q9L6Y7	09A	Q6VCY4
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	Match Length		275	271	283	283	285	285	271	282	282	282	282	283	282	304	304	283	280	283	283	280	285	279	279	282	282	282	282	283	281	282
ا ع مد	Match	100.0	99.3	83.3	63.0	63.0	62.2	62.2	59.7	36.6	36.4	36.4	36.1	35.9	35.9	35.9	35.9	35.8	35.5	35.4	35.4	35.2				32.7	32.6	32.6	32.4	32.3		32.1
	Score	. 4	1424	1194	903	903	892	892	856	525.5	522.5	522.5	517.5	515	514.5	514.5	514.5	514	509.5	507	507	504.5	494	489	482	469	467	467	464	463	460	460
1	REBUTC No.	-	N	e	4	'n	y	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

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	ehrlichia	ehrlichia	ehrlichia	ehrlichia	ehrlichia								
CATED	Q916y2	Q9adv9	Q9adv4	Q9adw1	Q9acj0	05fg16	Q410c1	Q9£477	Q93dd4	Q9zgj2	Q410c6	Q6vcy3	Q5ha15
73_EHRCH	12 EHRCH	19 EHRCA	14 EHRCA	W1_EHRCA	JO_EHRCH	L6_EHRRG	C1_EHRRU	77 EHRCA	Q93DD4 EHRCH	12 EHRCA	26 EHRRU	r3_EHRRU	15_EHRRW
09L63	09160	09AD	09AD	O9AD	O9AC	OSFGI	04100	09F4	093DI	9260	04100	06VC	Q5HA:
298 2	300 2	289 2	294 2	278 2	291 2	290 2	290 2	293 2	275 2	288 2	283 2	283 2	283 2
31.8	31.2	31.1	30.9	30.8	30.7	30.5	30.5	30.5	30.4	30.4	29.8	29.8	29.8
455.5	447.5	446	442.5	442	440	437.5	437.5	437	436	435.5	428	428	428
		4	u	9	_	00	0		41	~	m	4	2

# ALIGNMENTS

RESULT Q9F471	1 EHRCA
e e	Q9F471 EHRCA PRELIMINARY; PRT; 271 AA.
	27.17.1. 01.188.2001 (TrEMBLrel. 16, Created) 01.188.2001 (TrEMBLrel. 16, Created)
i i	(TrEMBLrel. 17, Last
	P28-9.
Z :	Name=p28-9;
	Burilcula camis. Bacteria: Proteobacteria: Alphaproteobacteria; Rickettsiales;
	Anaplasmataceae; Ehrlichia.
ž ŏ	NCBI_TaxID=944;
	lij NUCLEOTIDE SEQUENCE.
	STRAIN=Jake;
	MEDLINE=99242757;
¥ £	a conserved major i
	canis: a pot
	100017000
R E	Clin. Diagn. Lab. Immunoi. 6:392-399(1999). [3]
	LZ) NUCLEOTIDE SEQUENCE.
	STRAIN=Jake;
	MEDLINE=20432107; PubMed=10974556; DOI=10.1016/S0378-1119(00)00256-0;
_	McBride J.W., Yu X.J., Walker D.H.;
X C	pze mutrigene rocus
	Gene 254:245-252 (2000)
	EMBL; AF082744; AAG14363.1; -; Genomic_DNA.
	Pro, IPR002566; Surfa
og S	SEQUENCE 271 AA; 30374 MW; 8C8F22BB1D05B3EE CRC64;
Que	100.0%; Score 1434; DB 2; Length 271; nilarity 100.0%; Pred. No. 1.2e-109;
Mat	vat
à	1 MNYKRFVVGVILSTFVFFLSDGAFSDANFSEGRRGLYIGSQYKVGIPNFSNFSAEETIPG 60
đ	1 MNYKREVVGVTLSTEVFFLSDGAFSDANFSEGRRGLYIGSQYKVGIPNFSNFSAEETIPG 60
ò	61 ITKKIFALGLDKSEINTHSNFTRSYDPTYASSFAGFSGIIGYYVNDFRVEFEGSYENFEP 120
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3	
ò	121 ERQWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVCYDIASGSIPLAPYM 180
qq	121 ERQWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVCYDIASGSIPLAPYM 180
ò	181 CAGYGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVEIAXHP 240
qq	181 CAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVELAXHP 240

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Ohashi N., Unver A., Zhi N., Rikihisa Y.;
"Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins of Bhrlichia canis and application of the recombinant protein for serodiagnosis.";
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Anaplasmataceae, Ehrlichia.
NCBI_TaxID=944;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21153566; PubMed=11254561;
DOI=±0.1128/IAI.69-4.2083-2091.2001;
Ohashi N., Rikihisa Y., Unver A.,
"Analysis of transcriptionally active gene clusters of ma membrane protein multigene family in Ehrlichia canis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect. Immun, 69:2083-2091(2001).

EMBL; AF078553; AAK28700.1; -; Genomic_DNA.

InterPro; IPRO02565; Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_2; 1.

SEQUENCE 275 AA; 30843 WW; 3D8FD88FE507CE51 CRC64;
                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Majox outer membrane protein P30-20.
                                                                                                                                                                                                                                                                     275 AA
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                                                                   241 TALSDVPRTTSASATLNTDYFGWEIGFRFAL 271
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                            241 TALSDVPRTTSASATLNTDYFGWEIGFRFAL
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                                                                                                                                                                                                                                                              Q9ADV2 EHRCA PRELIMINARY;
Q9ADV2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269; Conservative
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ID 0691
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271 AA.

PRT;

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                                                                                                                                                                                                                                                                                                                MEDLINE=99175287; PubMed=10074538;
Yu X.J., McBride J.W., Walker D.H.;
"Genetic diversity of the 28-Kilodalton outer membrane protein gene
"human isolates of Bhrlichia chaffeensis.";
J. Clin. Microbiol. 37:1137-1143(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21153566, PubMed=11254561,
DOI=10.1128/IAI.69.4.2083-2091.2001;
Dohabhi N., Rikihisa Y., Unver A.;
"Analysis of transcriptionally active gene clusters of major outer membrane protein multigene family in Ehrlichia canis and E. chaffeensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu X.J., McBride J.W., Zhang X., Walker D.H.; "Characterization of the complete transcriptionally active Ehrchaffeensis 28 kDa outer membrane protein multigene family.";
                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Bhrlichia.
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26 271 P28-20.
271 AA; 30050 MW; 84EDF665DF3DB61C CRC64;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
P28-20 precursor (Major outer membrane protein P28-1)
Name=p28-20; Synonyms=p28-1;
Ehrlichia chaffeensis.
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Matches 213; Conservative 33; Mismatches
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EMBL; U72291; AAK28674.1; -; Genomic DNA.
InterPro; IPR002566; Surface Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TALSDVPRTTSASATLNTDYFGWEIGFRFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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10-MAY-2005 (TrEMBLrel. 30,
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ID QSFGQG EHRRG PRELIMINARY;
AC QSFGQG;
DT 10-MAY-2005 (TEMBLrel. 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 248:29-68(2000)
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                                                                                                                                                                                                                                                                                             STRAIN=Arkansas;
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                                                                                                                                                                                                              NCBI_TaxID=945;
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OSFGQ6 EHRRG
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Allsopp B.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GLTKGVYGLDLDLSKSDITKRANFTRLYNPTYSTSSTGIGGMFGYYFDNIRMEFETSYSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEPEROWYPENSOSYKFFALSRNAT ----NSDNKFIVLENNGVVDKSLNVNVCYDIASG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                 Prutos R., Ferraz C., Bensaid A., Eychenie S., Kandassami Y.,
Chantal I., Morgat A., Coissac E., Vachiery N., Demaille J., Viari A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNYKRPVVGVTLSTFVP-FLSDGAFSDANFSEGRRGLYIGSQYKVGIPNFSNFSAEETIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 MNYKEFVLGVTLSALLFSLLPQRAISDMDVSENRSRFYAGVQYRTGIPNFDNFSASETIP
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Anaplasmataceae, Ehrlichia.
NCBI_TaxID=779;
                                                 Mapl-related protein.
OrderedLocusNames=ERGA_CDS_09170;
Ehrlichia ruminantium [Strain Gardel].
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
NABAlsmantaceae; Ehrlichia.
NCBI_TaxID=302409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 283;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martinez D;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR955677; CAI28369.1; -; Genomic_DNA.
InterPro; IPR002566; Surface_Ag_msp4.
Complete proteome.
SEQUENCE 283 AA; 31817 MW; A7A918B9BBA22228 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update) 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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63.0%; Score 903; DB 2;
Best Local Similarity 59.5%; Pred. No. 5.6e-66;
Matches 166; Conservative 46; Mismatches 59.
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Ehrlichia ruminantium (Cowdria ruminantium)
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STRAIN-Gardel;
                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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Matches 166;
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1 MNYKRPVVGVTLSTFVF-FLSDGAFSDANFSEGRRGLYIGSOYKVGIPNFSNFSAEETIP

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                                                                                                                                                             173 SIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHE 232
                                                                                                                                                                                                                                     GITKKIFALGLD--KSEINTHSNFTRSYDPTYASSFAGFSGIIGYYVNDFRVEFEGSYEN 117
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                                                                                                                                       118 FEPERQWYPENSQSYKFFALSRNAT ----NSDNKFIVLENNGVVDKSLNVNVCYDIASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of a major outer membrane protein multigene family in Ehrlichia ruminantium.";
Gene 330:159-168(2004).
EMBL; AY343331; AAR10946.1; -; Genomic_DNA.
InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface Ag_2 2; 1.
SEQUENCE 285 AA; 32108 MW; 05E4C4E59A6F9118 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Ehrlichia.
NCBI_TaxID=779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 285;
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STRAIN=Welgevonden;
van Heerden H., Collins N.E., Brayton K.A., Rademeyer
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                                                                                                                                                                                                                                                                                                                      05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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59.1%; Pred. No. 4.5e-65;
iive 45; Mismatches 60;
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Best Local Similarity 59.1%
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSHA08 EHRRW PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                               QGVCX5_EHRRU PRELIMINARY;
QGVCX5;
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QSHA08 EHI
ID QSHA0
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Best Local Similarity 59.04
Matches 160; Conservative
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                                                                                          Gene 285:193-201(2002).
                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGSIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDR 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGIERQWYPEGSQSHKFCAVSRQDNAAPNTDSSNNNDFVVLENNGVKIRTLHVNFCYDVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 MNYKEFVLGVTLSALLFSLLPERAISDMDVSENRSRPYAGVQYRTGIPNFDNFSASETIP 64
                                                                                                                                                                                                                                                                                          Frutos R., Ferraz C., Bensaid A., Eychenie S., Kandassami Y.,
Chantal I., Morgat A., Coissac E., Vachiery N., Demaille J., Viari A.,
Martinez D.;
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                                                                                                                                                   PubMed=15637156; DOI=10.1073/pnas.0406633102;
Collins N.E., Liebenberg J., de Villiers B.P., Brayton K.A., Louw B., Pretorius A., raber P.E., van Heerden H., Josemans A., van Kleef M., Steyn H.C., van Strijp M.F., Zweygarth E., Jongejan F., Maillard J.C., Allsopp M.T., Allsopp B.A.;
"The genome of the heartwater agent Ehrlichia ruminantium contains multiple tandem repeats of actively variable copy number.";
Proc. Natl. Acad. Sci. U.S.A. 102:838-843(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
          10-WAY-2005 (TrEMBLrel. 30, Created)
10-WAY-2005 (TrEMBLrel. 30, Last sequence update)
110-MAY-2005 (TrEMBLrel. 31, Last annotation update)
Putative outer membrane protein MAP1+1 (Map1 related protein).
Name-map1+1, OrderediocusNames-ERWE CDS 09260, Erum8750,
ENTlichia ruminantium (strain Welgevonden).
Bacteria, Proteopbacteria, Alphaproteobacteria; Rickettsiales;
Anaplasmatacese; Ehrlichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 285;
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                                                                                                                                                                                                                                                                                                                                     (NOV-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 YDRVKVVYHPVQLNTVPKMTFVSANLDIDYFGCEVGIRFFL 285
                                                                                                                                                                                                                                                                                                                                                                                                              285 AA; 32108 MW; 05E4C4E59A6F9118 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 HERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRFAL 271
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      62.2%; Score 892; DB 2; 59.1%; Pred. No. 4.5e-65;
                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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13-SEP-2005 (TrEMBLrel. 31, Last sequence up
13-SEP-2005 (TrEMBLrel. 31, Last annotation
MAP1+1 (Fragment).
Mame=map1+1;
Ehrlichia ruminantium (Cowdria ruminantium)
                                                                                                                                                                                                                                                                                                                                               EMBL; CR925678; CA127420.1; -; Genomic_DNA.
EMBL; CR925678; CA127420.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
Complete proteome:
SEQUENCE 285 AA; 32108 MW; 05E4C4E
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Q4W4W3;
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                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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                                                                                                                  NCBI_TaxID=254945;
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CAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVEIAYHP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Senegal;
MEDLINE=22035368; PubMed=12039046; DOI=10.1016/S0378-1119(02)00408-0;
Bekker C.P., Bell-Sakyi L., Paxton E.A., Martinez D., Bensaid A.,
MEDLINE=22035368; PubMed=12039046; DOI=10.1016/S0378-1119(02)00408-0; Bekker C.P., Bell-Sakyi L., Paxton B.A., Martinez D., Bensaid A.,
                                                                                         Transcriptional analysis of the major antigenic protein 1 multigene
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                                                                                                                                                                                                                                     STRAIN=Senegal;
PubMed=1595193; DOI=10.1128/JB.187.14.4782-4791.2005;
Bekker C.P., Postigo M., Taoufik A., Bell-Sakyi L., Ferraz C.,
Bartinez D., Jongejan P.;
"Transcription Analysis of the Major Antigenic Protein 1 Multigene
Family of Three In Vitro-Cultured Ehrlichia ruminantium Isolates.",
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 271;
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Bekker C.P.J., Taoufik A., Jongejan F.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF319940; AAYS9059.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 AA; 30060 MW; F6AB82905DAA7680 CRC64;
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                                                                                                                     of Cowdria ruminantium.";
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Query Match
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PubMed=15637156; DOI=10.1073/pnas.0406633102;
Collina N.E., Liebenberg J., de Villiers E.P. Brayton K.A., Louw E.,
Pretorius A., Faber F.E., van Heerden H., Josemans A., van Kleef M.,
Steyn H.C., van Strijp M.F., Zweygarth E., Jongejan F., Maillard J.C.,
Berthier D., Botha M., Joubert F., Corton C.H., Thomson N.R.,
Allsopp M.T., Allsopp B.A.,
"The genome of the heartwater agent Ehrlichia ruminantium contains
multiple tandem repeats of actively variable copy number.";
Proc. Natl. Acad. Sci. U.S.A. 102:838-84312005).
EMBL: CR767821; CA458608.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                STRAIN=Senegal;
Pubmed=15995193; DOI=10.1128/JB.187.14.4782-4791.2005;
Pubmed=159595193; DOI=10.1128/JB.187.4.5847i L., Ferraz C.,
Martinez D., Jongejan F.;
Martinez D., Jongejan F.;
Transcription Analysis of the Major Antigenic Protein 1 Multigene
"Transcription Los Cultured Bhrlichia ruminantium Isolates.";
J. Bacteriol. 187:4782-4791(2005).
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Bacteria, Froteobacteria, Alphaproteobacteria, Rickettsiales,
Anaplasmataceae, Ehrlichia.
NCBI_TaxID=254945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 282;
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                                                                                                                                                                                                                                                                                                                                                                            TNCLEACH SENEGAL;
STRAINS-SENEGAL;
Bekker C.P.J., Taoufik A., Jongejan F.;
Bekker C.P.J., Taoufik A., Jongejan F.;
Bubmitted (NOV-2004) to the EMBL/GenBant/DDBJ databases.
EMBL; AF319940; AAV54088.2; -; Genomic DNA.
SENDLNCE 282 AA; 31097 MW; 3D619510E7393EBB CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Putative outer membrane protein MAPI-1.
Name=map1-1; OrderedLocusNames=Erum8730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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41.8%; Pred. No. 6.1e-35;
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InterPro; IPR012566; Surface Ag msp4.
InterPro; IPR011991; Wing hlx DNA bd.
Pfam, PF01617; Surface Ag_2; I.
Complete proteome.
SEQUENCE 282 AA; 31100 MW; ICB2DA
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Best Local Similarity 41.8%
Matches 120; Conservative
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QSHA10;
                              NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                         55 BET----IPGITKKIFALGLDKSEINTHSNFTRSYDPTYASS---FAGFSGIIGYYVNDF 107
                                                                                                                                                                                                                                                                                        108 RVEFEGSYENFEPERQWYPEN----SQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNV 163
                                                                                                                                                                                                                                                                                                                                                                                           222
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                                                                                                                          1 MNYKRFVVGVTLSTFVFFLSDGAFSDANFS-----EGRRGLYIGSQYKVGIPNFSNFSA
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                                                                                                                                                                                                                                                                                                                                                                                           164 NVCYDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of a major outer membrane protein multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a multigene
                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99216274; PubMed=10198207; DOI=10.1006/bbrc.1999.0459; Sulsona C.R., Mahan S.M., Barbet A.F.; "The mapl gene of Cowdinia ruminantium is a member of a multiger family containing both conserved and variable genes."; Biochem. Biophys. Res. Commun. 257:300-305(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Bhrlichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.4%; Score 522.5; DB 2; Length 282;
Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 YHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Welgevonden;
van Heerden H., Collins N.E., Brayton K.A., Rademeyer C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                Indels
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Gene 330:159-168(2004).

Gene 330:159-168(2004).

EMBL; AF125275; AAD26345.1; -; Genomic_DNA.

EMBL; AF125275; AAD26345.1; -; Genomic_DNA.

EMBL; AY343331; AAR10944.1; -; Genomic_DNA.

InterPro; IPR002566; Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_msp4.

SEQUENCE 282 AA; 31100 WW; 1CB2DA256B2CA990 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
13.SEP-2005 (TrEMBLrel. 31, Last annotation update)
Major antigenic protein 1 like protein (WAP1-1).
Ehrlichia ruminantium (Cowdria ruminantium).
                                                  95;
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  DB 2;
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     Query Match
Best Local Similarity 41.8%; Pred. No. 1.1e-34;
Matches 120; Conservative 47; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
  Score 522.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=779;
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Length 283;

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EET-IPG---ITKKIFALGLDKSEINTHSNFTRSYDPTYA---SSFAGFSGIIGYYVNDF 107
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                                                                                                                     MEDLINE=22384137; PubMed=12496165; DOI=10.1128/IAI.71.1.187-195.2003; Cheng C., Paddock C.D., Ganta R.R.; Cheng C., Paddock C.D., Ganta R.R.; Wolecular heterogeneity of Ehrlichia chaffeensis isolates determined by sequence analysis of the 28-kilodalton outer membrane protein genes and other regions of the genome."; Infect. Immun. 71:187-195(2003).

EMBL; AR479813; AA012959.1; -; Genomic DNA.

EMBL; AR479840; AA012955.1; -; Genomic_DNA.

EMBL; AR4798102565; Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_msp4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EETPINGNTAITKKVFGLKKD-GDIAQHGDFTRT-DPALEFQNNLISGFSGSIGYAMDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNYKRFVVGVTLSTFVFFLSDGAF-----SDANFSEGRRGLYIGSQYKVGIPNFSNFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVEFEGSYENFEPERQWYPENSQS-----YKFFALSRNATNSDNKF1VLENNGVVDKSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 VNVCYDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNYKRFVVGVTLSTFVFFLSDGAFSDANFS-----EGRRGLYIGSQYKVGIPNFSNFSA
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Anaplasmataceae, Ehrlichia.
NCBI_TaxID=945,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Gardel,
Martinez D., Ferraz C., Demaille J., Bensaid A., Frutos
"Analysis of the major antigenic protein 1 multigene fam
Ehrlichia ruminantium strain Gardel.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY652746; AAV73824.1; -; Genomic DNA.
SEQUENCE 282 AA; 31052 MW; OCB3C649A691BC90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       Query Match
35.9%; Score 515; DB 2; L.
Best Local Similarity 40.3%; Pred. No. 4.5e-34;
Matches 116; Conservative 49; Mismatches 97;
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                                                                                                          SEQUENCE
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Best Local Simil
Matches 119; (
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EHRRU
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                     RVEFEGSYENFEPERQWYPEN----SQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNV 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99216274; PubMed=10198207; DOI=10.1006/bbrc.1999.0459; Sulsona C.R., Mahan S.M., Barbet A.F.;
Sulsona C.R., Mahan S.M., Barbet A.F.;
The mapl gene of Cowdria ruminantium is a member of a multigene family containing both conserved and variable genes.";
Biochem. Biophys. Res. Commun. 257:300-005(1999).
EMBL; AF125279; AAD26353.1; ; Genomic_DNA.
EMBL; AR125277; AAD26343.1; ; Genomic_DNA.
EMBL; AR125279; AAD26343.1; ; Genomic_DNA.
EMBL; AR125279; SAD26343.1; ; Genomic_DNA.
InterPro; IPR002566; Surface Ag_msp4.
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                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-FBB-20005 (TrEMBLrel. 29, Last annotation update)
Major antigenic protein 1 like protein.
Enrilchia tuminantium (Cowdria ruminantium).
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Anaplasmatecee, Ehrlichia.
NCBI_TAXID=779;
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                                                                                                                                                                                      YHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                                                                 YHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01617; Surface Ag_2; 1. SEQUENCE 282 AA; 31040 MW; 0CB3C655775CBC90 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
28kDa outer membrane protein gene 14.
Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.1%; Score 517.5; DB 2
41.5%; Pred. No. 2.8e-34;
ive 47; Mismatches 96
                                                                                                                                                                                                                                                                                                              Q9R443 EHRRU PRELIMINARY;
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Matches 119; Conservative
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Q8G812;
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                                                                                                                                                                                                                                                                                                       234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 RVEFEGSYENFEPERQWYPEN----SQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNV 163
108 RVEFEGSYENFEPERQWYPEN----SQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNV 163
                                                                                                                                           164 NVCYDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGGY 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frain-Gardel;
Frutos R., Ferraz C., Bensaid A., Eychenie S., Kandassami Y.,
Frutos R., Ferraz C., Bensaid A., Eychenie S., Kandassami Y.,
Frutos R., Ferraz C., Bensaid B., Vachiery N., Demaille J., Viari A.,
Martinez D.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
ENBL; CR925677; CAI28367.1; -; Genomic_DNA.
Interpro; IPR002566; Surface_Ag_msp4.
Fram; PF01617; Surface_Ag_2; 1.
Complete proteome.
SEQUENCE 304 AA; 33925 MW; 009338D2B65AE800 CRC64;
                                                                                                                                                                                                                                                                           25; Gaps
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Mapl-related protein.
Ordered
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Best Local Similarity 41.5%; Pred. No. 5.3e-34;
Matches 119; Conservative 46; Mismatches 97; Indels
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COFFGL4 ERRRG
COFFGL4 EN COFFGL4 E
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OM protein - protein search, using sw model

December 28, 2005, 15:05:48; Search time 25 Seconds (without alignments) 1042.990 Million cell updates/sec Run on:

US-10-731-554-46 1434 1 MNYKRFVVGVTLSTFVFFLS.......ASATLNTDYFGWEIGFRFAL 271 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	28k surface antige	28k surface antige	major antigenic pr	28k surface antige	Burface	28k surface antige	major surface prot	28k surface antige	iron(III) dicitrat	heat resistant agg	iron (III) dicitra	hypothetical prote	probable TonB syst	conserved hypothet	toxin-like outer m	cell surface glyco	vacuolating cytoto	toxin-like outer m	hypothetical prote	vacuolating cytoto		hypothetical prote	toxin-like outer m	probable outer mem	hypothetical prote		NADH2 dehydrogenas	flagellin chain B	opacity protein op
SUMMAKIES	ΩI	JE0217	JE0216	I40882	JE0220	JE0219	JE0218	I39648	JE0221	G64620	AG3556	F71894	E70120	F82506	B71315	B64596	A48832	B53739	D71917	E64483	S44983	F90257	T31287	H71879	AH0541	T19515	875309	T12716	B32808	S36343
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	Length	280	278	284	287	286	276	282	133	787	284	792	614	713	991	1943	730	1287	3194	624	1291	637	726	2399	239	460	1118	736	396	237
dŧ	Query Match	29.3	27.7	26.7	26.4	26.4	26.3	19.4	10.2	7.1	7.0	6.9	6.8	6.9	6.8	6.7	6.7	9.9	6.5	6.5	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.3	6.3	6.3
	Score	419.5	397.5	383.5	379	378.5	377	278	146.5	102	100	66	97.5	97.5	97.5	96.5	96	95	93.5	93	93	92.5	92.5	92.5	91.5	91.5	91.5	91	90.5	90
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ABSULT 2
28k surface antigen 3 - Ehrlichia chaffensis
28k surface antigen 3 - Ehrlichia chaffensis
NiAlcernate names: MAP1
C;Species: Bhrlichia chaffensis
C;Sacession: JE0216
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem Biophys Res. Commun. 247, 635-643, 1998
A;Title: Molecular characterization of a 28bos surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180; PMID:9647746

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	probable hydroxama	hydroxamate-type f	hypothetical prote	probable membrane	hypothetical prote	. triacylglycerol li	hypothetical prote	outer membrane pro	hypothetical prote	conserved membrane	hypothetical prote	IgA-specific metal	IgA-specific metal	hypothetical prote	N-cadherin precurs	CS3 pilin synthesi
	C98235	A13050	S58108	S53378	B71685	A34671	G90604	A71907	D71621	AE1514	T40953	A26039	S61314	140765	150116	S78561
	~	~	7	~	7	-	~	N	7	~	7	~	~	~	~	7
	710	716	1101	1769	298	482	493	270	797	968	926	1532	1561	374	783	937
	6.3	6.3	6.3	6.3	6.2	6.2	6.2	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1
•	90	90	06	06	83	89	89	88.5	88	87.5	87.5	87.5	87.5	87	87	87
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 280217 28k surf. N;Altern C;Specie C;Acces C;Acces R;Reddy, Bjochem. A;Refere A;Refere A;Residu A;Residu A;Cross-	RESULT 1 JUNE 11 JUNE 217 JUNE 218 JUNE 218 JUNE 218 JUNE 21988 SETT 11 JUNE 21998 SETT 11 JUNE 21 JUNE 21998 SETT 11 JUNE 2199
Query Best L Matche	Query Match 29.3%; Score 419.5; DB 2; Length 280; Best Local Similarity 34.1%; Pred. No. 1.2e-27; Matches 98; Conservative 59; Mismatches 103; Indels 27; Gaps 7;
y d	1 MNYKRFVVGVTLSTFVFFLSDGAFSDANFSEGRRG-LVIGSQYKVGIPNFSNFSAEETIP 59     :  :     : :     : :       : :       : :         : :         : :         : :         : :         : :         : :         : :         : :         : :         : :         : :             : :
& <b>4</b>	60 GITKKIFALGLDKSBINTHSNFTRSYDPTVASSFAGFSGIIGYYVNDFRVFFE 112
& 43	113 GSYENFEPERQWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVCYD 168          : :
<b>ራ</b> ብ	169 IASGSIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFCGGYYHKVVG 228 :
& 8	229 DRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269 : :      : :      : :      240 NBFRDIPAMIPSTSTLTGNHFTIVTLSVCHFGVELGGRF 278

tribe A.R.

셤 ઠે 셤 ò g δ 셤 ò 원

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A;Cross-references: UNIPROT:Q9ZGJO; UNIPARC:UPI0000034790; GB:AF062762; NID:g3327964; P11
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NyAlternate names: MAPI
NyAlternate names: MAPI
S'Species Bhrlichia chaffensis
C'Species Bhrlichia chaffensis
C'Species Bhrlichia chaffensis
C'Species Bhrlichia chaffensis
C'Species Shringer 1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C'Accession: JE0219
C'R. Sulsons C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys Res. Commun. 247, 613-643, 1998
A;Title: Molecular characterization of a 2845 surface antigen gene family of the tribe A;Reference number: JE0216; MUID:98321180; PMID:9647746
                                                                               C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JB6220
R;Reddy, G.R.; Bulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, Blochem. Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the A;Reference number: JB6216; MUID:98321180; PMID:9647746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -QSFTKVL---VGLDQRLSHNIINNNDTAKSLKVQNYSFKYKNNPFLGFAGAIGYSIGNSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 NTTVGVFGIEQDWDRCVISRTTLSDIFTVPNYSFKYE---NNLFSGFAGALGYSMDGPRI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 IPGITKKIFALGLDK----SEINTH----SNFTRSYDPTYASS-FAGFSGIIGYYVNDFR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 VEFEGSYENFEPERQWYPENSQSYKFFALSRNA------TNSDNKFIVLENNGV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 VDKSLNVNVCYDIASGSIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GITKKIFALGLD------KSEINTHSNFTRSYDPTYASSFAGFSGIIGYYVNDFRV 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKYKKTFTVTALVLLISFTHFIP--FYSPARAST-IHNFYISGKYMPTASHFGIFSAKEE 57
                           28k surface antigen 1 - Ehrlichia canis
C;Species: Ehrlichia canis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFEGSYENFEPERQWYPENSQSYKFFALSR------NATNSDNKFIVLENNGVVDKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFGGGYYHKVVGDRHERVEIAYHPTAL --- SDVPRTTSASATLNTDYFGWEIGFRF
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A;Residues: 1-286 <RED>
A;Cross-references: UNIPROT:052105; UNIPARC:UPI000003478C; GB:AF062761
                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.4%; Score 379; DB 2; Length 28 Best Local Similarity 34.1%; Pred. No. 3e-24; Matches 101; Conservative 55; Mismatches 102; Indels
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A, Molecule type: DNA
A, Residues: 1-287 <RED>
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Best Local Simil
Matches 93; (
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C;Species: Cowdria ruminantium (heartwater rickettsia)
C;Species: Cowdria ruminantium (heartwater rickettsia)
C;Species: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: 140882; S42827
R;van Vliet, A.H.; Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.
R;van Vliet, A.H.; Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.
A;Reference number: 140882; MUD:94178956; PMID:8132352
A;Accession: 140882
A;Accession: 140882
A;Accession: 140882
A;Accession: 140882
A;Residus: 1-284 <RES>
A;Residus: 1-284 <RES>
C;Genetics:
A;Gene: mapl
                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                      PGITKKIFAL----GLDKSEINTHSNFTRSYDPTYASS-FAGFSGIIGYYVNDFRVEFE 112
                                                                                                                                                                                                                                                                                                                                                                                                                              GSYENFEPERQWYPENSQSYKFFALSRNATN---SDNKFIVLENNGVVDKSLNVNVCYDI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASGSIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGITKKIFAL----GLDKSBINTHSNFT-RSYDPTYASS-FAGFSGIIGYYVNDFRVEF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGSYENFEPEROW--YPENSOSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVCYDI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 MLDGMPVSPYVCAGIGTDLVSVINATNPKLSYQGKLGISYSINPEASIFIGGHFHRVIGN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASGSIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGD 229
                                                                                                                                                                                                                    28
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                                                                                                                                                                                                                                                  1 MNYKRFVVGVTLSTFVFFLSDGAFSDANFSEGRRG-LYIGSQYKVGIPNFSNFSA-EETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNYKRFVVGVTLSTFVFFLSDGAFSDANFSEGR--RGLYIGSQYKVGIPNFSNFSAEETI
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
A;Molecule type: DNA
A;Residues: 1-278 <RED>
A;Cross-references: UNIPROT:O52106; UNIPARC:UP1000003478D; GB:AF062761
                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.7%; Score 383.5; DB 2; Length 284; 32.9%; Pred. No. 1.2e-24; ive 55; Mismatches 120; Indels 15;
                                                                                                             Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFRDI -----PTLKAFV--TSSATPDLALVTLSVCHFGIELGGRF 276
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHERVEIAYHPTALSDVPRTTS---ASATLNTDYFGWEIGFRF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFKDIATSKVFTSSGNASSAVSPGFASAILDVCHFGIEIGGRF 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHERVEIAYHPTALSDVPRTTSAS-----ATLNTDYFGWEIGFRF
                                                                                                          27.7%; Score 397.5; DB 2;
34.7%; Pred. No. 8.1e-26;
iive 55; Mismatches 106;
                                                                                                                                  Best Local Similarity 34.7%
Matches 99, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                              113
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A,Accession: JE0221
A,Molecule type: DNA
A,Residues: 1-133 <RED>
A,Cross-references: UNIPROT:O85360; UNIPARC:UPI0000034791; GB:AF062762; NID:g3327964; Pli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species Helicobacter pylori
C; Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C; Accession: G64620
R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A; Athathors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; A; Accession: G64620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:025487; UNIPARC:UP10000003029; GB:AE000592; GB:AE000511; NID; Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sek surface antigen 2 - Ehrlichia canis
C;Species: Ehrlichia canis
C;Species: Landis acanis
C;Accession: 1908 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE021
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, Biochem. Biophys. Res. Comun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the A;Reference number: JE0216; MUID:98321180; PMID:9647746
                                                                                                          116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 PGITKKIFALGLDK-----SEINTHSNFT-RSYDPTYASS-FAGFSGIIGYYVNDFRV 109
                                                                                                                                                                                         103 YVNDFRVEFEGSYENFEPEROWYPENSOSYKFFALSRNATNSDNKFIVLENNGVVDKSLN 162
                                                     SNFSAEETIPGITKKIFALGLDKS----EINTHSNFTRSYDPTYASS---FAGFSGIIGY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-787 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 VNVCYDIASGSIPLAPYMCAGVGADYIKPLGISLPKFSYQVKFGVNYPLNVNTMLFGGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNYKR-FVVGVTLSTFVFFLSDGAFSDANFSEGRRG-LYIGSQYKVGIPNFSNFSAEETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNYRELFTGGLSAATVCACSLLVSGAVVASPMSHEVASEGGVMGGSFYVGAAYSPAFPSV
                                                                                                     61 TSPDMRES---SKETSYVRGYDKSIATIDVSVPANFSKS-GYTFAFSKNLITSFDGAVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iron(III) dicitrate transport protein - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  223 YHKVVGDRHERVEIAYHPTALSDVPRTTS-----ASATLNTDYFGWEIGFRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:025487; UNIPARC:UPI0000033029; C;Superfamily: ferrichrome-iron receptor; tonB-dependent reC;Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%; Score 146.5; DB 2;
llarity 33.6%; Pred. No. 3e-05;
Conservative 23; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 102; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%;
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EVEMSYEAFDVKNQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 EFEGSYENFEPERO 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity
45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
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C;Species: 19-011-1996
B;Space: 13-011-1996
B;Space: 139648
B;Oberle, S.M.; Barbet, A.F.
G;Accession: 139648
B;Oberle, S.M.; Barbet, A.F.
A;Accession: 139648
A;Title: Derivation of the complete msp4 gene sequence of Anaplasma marginale without classerance number: 139648
B;Accession: 139648
B;Accession: 139648
B;Accession: 139648
B;Accession: 139648
B;Accession: 1292 <RES>
B;Residues: 1-282 <RES>
B;Residues: 1-282 <RES>
B;Crosser-references: UNIPROT:Q07408; UNIPARC:UPI000000B7F; GB:L01987; NID:g142174; PIDN: A;Gene: msp4
                                                                                                                                                                                                                                                 JE0218
JE0218
Suk surface antigen 5 - Ehrlichia chaffensis
N.Alternate names: MAP1
C;Species: Ehrlichia chaffensis
C;Species: Ehrlichia chaffensis
C;Species: Lang-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0218
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
B;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
A;Reddy, G.R.; Sulsona, Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28Mbs surface antigen gene family of the tribe A;Reference number: JE0216; MUID: 98321180; PMID: 9647746
A;Reference number: DNA
A;Residues: 1-276 <RED>
A;Residues: 1-276 <RED>
A;Residues: 1-276 <RED>
A;Cross-references: UNIPROT: Q93DD2; UNIPROT: Q9AC19; UNIPARC: UPI000003478F; GB: AF062761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 FEGSYENFEPERQWYPENSQSYKFFALSRNA----TNSDNKFIVLENNGVVDKSLNVNVC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDIASGSIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 TTVGVFGLKQNWDGSAISNSSPNDVFTVSNYSFKYE---NNPFLGFAGAIGYSMDGPRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNYKRFVVGVTLSTFVFFLSDGAFSDANFSEGRRGLYIGSQYKVGIPNFSNFSAEETIPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNYKKVFITSALISLISSLPGVSFSDPAGSGINGNFYISGKYMPSASHFGVFSAKEE-RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 19.4%; Score 278; DB 2; Length 282;
Best Local Similarity 26.1%; Pred. No. 8.2e-16;
Matches 77; Conservative 57; Mismatches 119; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNYKR-FVVGVTLSTF--VFFLSDGA----FSDANFSEG---RRGLYIGSQYKVGIPNF
                                                                                                                      YYHKVVGDRHERVEIAYHPTALSDVPRTTS-----ASATLNTDYFGWEIGFRF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGDRHERVEIAYHPTALSDVPRTTSASAT------LNTDYFGWEIG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.3%; Score 377; DB 2; Length 27 Best Local Similarity 29.8%; Pred. No. 4.2e-24; Matches 87; Conservative 57; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227
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tribe A.R.

Best Local Similarity 21.3%; Pred. No. 1.7; Matches 64; Conservative 44; Mismatches 138; Indels 54; Gaps 11;	R;Alm, R.A.; Ling	ភ ខ្លី
Qy 2 NYKRFVVGVTLSTFVFFLSDGAFSDANFSEGRRGLYIGSQYKVGIPNFSNFSAEETIP 59	A;Title: Genomic	7 5
Db 455 NGSGFDAGTSLNNFNNYTAVYASDEINFNNGMLTITPGLRYTFLNYEKKDAPPFK 509	A;Reference numbe A;Accession: F718	စ္ကုဆ
QY 60 -GITKKIFALGLDKSEINTHSNFTRSYDFTYASSFAGFSGIIGYYVND 106	A;Status: prelimi A;Molecule type:	귤
Db 510 AGTGKTIKDRYNQWNPAVNVGYKPIKELLFYFNYQRSYIPPQFSNIGSFVGTSTDYFQI 569	A;Cross-reference	92 95
Qy 107 FRVEFEGSYENFEPERQWYPENSQSYKFFALSRNATUSDNKFIVLE 152	A;Experimental sor C;Genetics:	õ
Db 570 FNVMEGGSRYYFNNQVSFNANYFVIFANNYFTGRYGDNKBPVNARSQGVELE 621	A;Gene: fecA_2 C;Superfamily: fe	[6]
QY 153 NNGVVDKSLNVNVCYDIASGSIPLAPYMCAGVGADYIKFLGISLPKFS-YQVKFG 206	Query Match	
Db 622 LYYTPIRGLNFHAAYTFIDANITSHTMVTNPANPKGPKKDIFGKKLPFVSPHQFILD 678	Best Local Simil Matches 65; (	넡
QY 207 UNYPLNUNTMLFGGGYYHKVVGDRHERVE-IAYHPTALSDVPRTTSASATLNTDYFGWEI 265	Qy 2 NYKG	S
Db 679 ASYTYAKTTIGLSSFFYSRTYSDVINTVPFIQYAPTIKNGAITKTAGMTPWYWVNL 736	Db 455 NGSC	ŠŠ
OT F.HISBE	75- 09 KO	H
AG3556 heat registant and utinin 1 proguesory (imposted) - progular and though (stanta 100)	Δ9Λ 01S	_င်္ဂ
Cypecies Brucella melitensis	Qy 107 FRVE	
C;Date: U1-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Ju1-2004 C;Accession: AG3556	   Db 570 FIVE	—≴
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess	Qy 158	S
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten	qQ	5
A;Reference number: AD3252; PMID:11756688		
A;Status: preliminary	717 AD	ž –
A;Molecule type: DNA A;Residues: 1-284 <kur></kur>	Db 684 AKT	Ē
A;Cross-references: UNIPROT:Q8YD01; UNIPARC:UPI0000058467; GB:AE008918; PIDN:AAL53618.1, A;Experimental source: strain 16M C;Genetics:		
A;Gene: BMEI10376 A;Map position: II	hypothetical prote C/Species: Borreli	7,4
7.0%; Score 100;	C;Date: 13-Feb-199 C;Accession: E7012	52
œ,	R;Fraser, C.M.; Cason, B.; Peterson,	ပ္ပိုင္ကို
Qy 82 TRSYDPTYASSFAGFSGIIGYYVNDFRVEFEGSYENFEP 120	; Bowman, C.; Gar] Nature 390, 580-58	2 33
TNCPSYVKSSHGLNPVE	A; Authors: Smith, A; Title: Genomic	
Ov 121 EROMYPENSOSYKFFALSRNATNSDNKFTVLFNNGVKNKSLNNNVCYDTASGSTDLADVM 180	A; Reference number	95
	A;Status: prelimin	141
	A;Residues: 1-614	4
ISI CAGUGADYIKK	A;Cross-references A;Experimental sou	9 0
7/1	Query Match	
223	Best Local Simil Matches 51; C	뒫
Db 232 YLRVNGGNAYGYDEQDRQVINQYGQGAGADGPQAKDNGFNIHTVRAĞLRYEFR 284	Qy 2 NYKH	Ä
RESULT 11	: RYYG 131 DY	二克
F71894 iron (111) dicitrate transmort protein - Helicoberter milori (etrain 100)		ř

iron (III) dicitrate transport protein - Helicobacter pylori (strain J99) C; Species: Helicobacter pylori A; Variaty: atrain J99 atrain J99 atrain J99 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004 C; Accession: F71894

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g, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
on, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; 7
180, 1999
                                                                                       sequence comparison of two unrelated isolates of the human gastric pathoer: A71800; WUID:99120557; PMID:9923682
894
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Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, M. J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, rland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, R.; Hatch, B.
                                                                                                                                                                                                                                                    2 <ARN>
es: UNIPROT:Q9ZL37; UNIPARC:UPI0000D3692; GB:AE001505; GB:AE001439; NID
ource: strain J99
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ource: strain B31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /BFEGSYENFEPERQWYPENSQSYKFFAL-----SRNATNSDNKFIVLENNGVV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLNVNVCY-----DIASGSIPLAPYMCAGVGADYIKFLGISLPKFS-YQVKFGVNYPL 211
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sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
br: A70100; MUID:98065943; PMID:9403685
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lia burgdorferi (Lyme disease spirochete)
998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 FSSGVYGDIFLISQKSGFIKKISFPFKKQIIRILDLSSKNVEKILVRTYDNHFYSYINGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRFVVGVTLSTFVFFLSDGAFSDANFSEGRRGLYIGSQYKVGIPNFSNFSAEETIP--
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llarity 25.5%; Pred. No. 2.9;
Conservative 26; Mismatches 78; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 -IPGITKKIFALG-------LDKSEINTHSNFTRSYDPTYASSFAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.9%; Score 99; DB 2; Length 792; ilarity 22.0%; Pred. No. 3; Conservative 40; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  < KLE>
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A;Molecule type: DNA
A;Residues: 1-991 <COL>
A;Cross-references: UNIPROT:083528; UNIPARC:UPI00000C0A89; GB:AE001227; GB:AE000520; NID
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cylore: Outer membrane protein HP0610 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession. B64596
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Attler: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B64596
A;Accession: B64596
A;Accession: preliminary; nucleic acid sequence not shown; translation not shown
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A;Residues: 1-1943 <TOM>
A;Cross-references: UNIPROT:025331; UNIPARC:UPI0000D30AD; GB:AE000575; GB:AE000511; NID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNYKRFVVGVTL-----STFVFFLSDGAFSDANFSEGRRGLYIGSQYKVGIPN 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            II: ||| || :: : ||| || || LINFGATVVGTLILLGSAQEKANNNGSIWFGKNNLLYLHONFN--ATNIFLTNNFNVGNPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTWG--GFNFNSGRITFENTTFSGWTNINGATESGSSYVNMVANTDLIFSNSILGGGIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 NVNVCYD-----IASGSIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVN--YPLN
                                                                                                                                                                                                                                                                                                             42 YKVGIPNFSNFSAEETIPGITKKIFALGLDKSEINTHSNFTRSYDPTYASSFAGFSGIIG
                                                                                                                                                                                                                                                                                                                                                                 723 YAYSIATFLSF-----PYISATLSARFLDKPOVRAELDFRMPYEITCKOT-----
                                                                                                                                                                                                                                                                                                                                                                                                                        102 YYVNDFRVEFEGSYENFEPERQWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSL
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Best Local Similarity 22.9%; Pred. No. 16;
Matches 62; Conservative 42; Mismatches 102;
                                                                                                                                                                                                                                                       94;
                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                Query Match 6.8%; Score 97.5; DB
Best Local Similarity 22.0%; Pred. No. 5.4;
Matches 51; Conservative 36; Mismatches
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                                                                                                                                                                                                                                                                                            C; Species: user victor vcavues unmoorted] - Vibrio cholerae (strain N16961 serogration vibro cholerae
C; Species: vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C; Accession: F82506
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Natture 406, 477-483, 2000
A; Ttle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Accession: F82506
A; Stevence number: A82035; MUID: 20406833; PMID: 10952301
A; Accession: F82506
A; Stevence vyee: DNA
A; Residues: 1-113 cHEI>
A; Cross-references: UNIPROT: Q9KNA1; UNIPARC: UPI00000C33F5; GB: AE004349; GB: AE003853; NIC
C; Genetics:
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McDo
                                                                                                                                                                                                                                                                                      probable TonB system receptor VCA0064 [imported] - Vibrio cholerae (strain N16961 serog:
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R)Fraser, C. (M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Chraser, C.M.; Norris, S.J.; Weinston, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; I trson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; I trson, J.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID:98332770; PMID:9665876
A; Reference number: A71250; MUID:98332770; PMID:9665876
A; Reference number: A71250; MUID:98332770; PMID:9665876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KIFALGLDK------SEINTHSNFTR----SYDPTYASSFAGFSGIIGYYVN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPRVEFEGSYENFEPERQWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNV-N 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------KPNNKLRAETSDS---FELGSKYDNGQTQFYVAVFYSIFDNFIDVKQ 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 VCYDIASGSIPLAPYMCAGVGADYIKFLGISLP-------KFSY-QVKFGVNYP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 VGYDNATGSVIQQYQNIAGV----KTYGAEMSVMHRLDDRWSVENKLGYVDGKDGENQY 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 LNVNTMLFGGGY--YHKVVGDRHERVEIAYHPTALSDVPRTTS----ASATLNTDYFGW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein TP0515 - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 C;Accession: B71315
        : | : | | | : | | : | ---QRMQLAXOKGSIYLTAYTLRNKKAVDERFKFIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DGAFSDANFSEGRRGLYIGSQYKVGIPNFSN-----FSAEETIPGITK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.8%; Score 97.5; DB 2; Length 713; Best Local Similarity 21.2%; Pred. No. 3.5; Matches 65; Conservative 36; Mismatches 116; Indels 8
                                                                                                                                 300 DSGMNAVVIDFKDDNGNLTY 319
                                                                                           NNG----VVD-KSLNVNVCY 167
        249 WVFIGKLSLQDQDF---FEKS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIGFRF 269
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OM protein - protein search, using sw model

December 28, 2005, 15:38:40 ; Search time 18 Seconds (without alignments) 112.748 Million cell updates/sec Run on:

Title: Perfect score:

US-10-731-554-46 1434 1 MNYRRFVVGVTLSTFVFFLS.......ASATLNTDYFGWEIGFRFAL 271 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

57103 segs, 7488799 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA\_New:\*

1: /cgn2\_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/PCT NEW PUB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:\*

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8: /cgn2\_6/ptodata/1/pubpaa/USIO\_NEW PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/USIO\_NEW\_PUB.pep:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		di			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
н	85	5.9	1565	9	US-10-467-657-2704	Sequence 2704, Ap
2	84	5.9	477	7	US-11-055-822-98	Sequence 98, Appl
e	83.5	5.8	1433	7	US-11-094-519A-40	Sequence 40, Appl
4	81	5.6	876	7	US-11-077-550-128	128
S	81	5.6	877	7	US-11-077-550-126	Sequence 126, App
9	81	5.6	877	7	US-11-077-550-130	130
7	81	5.6	881	7	US-11-077-550-124	124,
80	81	5.6	905	7	US-11-077-550-132	132,
6	81	5.6	912	7	US-11-077-550-116	116,
10	81	5.6	914	7	US-11-077-550-120	120
11	81	5.6	944	7	US-11-077-550-122	122
12	81	5.6	950	7	US-11-077-550-118	Н
13	78	5.4	219	7	US-11-170-653-29	59,
14	77.5	5.4	1122	7	US-11-191-374-3	۳,
15	77.5	5.4	1122	7	US-11-191-375-3	Sequence 3, Appli
16	77.5	5.4	1122	7	US-11-191-588-3	m
17	16	S.3	1296	9	US-10-615-668-3	(*)
18	16	5.3	1468	9	US-10-467-657-1088	ĩ
19	9/	5.3	2053	7	US-11-013-759-9	U,
20	75	5.2	1992	7	US-11-013-759-3	Sequence 3, Appli
21	75	5.2	1992	7	US-11-013-759-13	13
22	75	5.2	2047	,	US-11-013-759-4	4
23	75	5.2	2047	7	US-11-013-759-7	7,
24	74	5.2	826	9	US-10-793-626-1066	106
25	73	5.1	278	9	US-10-467-657-7386	Sequence 7386, Ap

187 LRDLSQAYRYAIAGTPYKDINIDQTWNTEGL---IGF 220

g

Sequence 1778, Ap Sequence 98, Appl Sequence 228, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequence 31, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 2512, Ap Sequence 2512, Ap Sequence 184, Appl Sequence 2512, Appl Sequence 184, Appl Sequence 184, Appl Sequence 184, Appl Sequence 2512, Ap Sequence 2512, Appl Sequence 2512, Ap	ì
US-10-467-657-1778 US-10-316-98 US-10-984-376-13 US-10-793-626-2286 US-11-120-543-18 US-11-120-543-18 US-11-170-653-30 US-11-170-653-31 US-10-984-376-8 US-11-170-653-31 US-10-984-376-8 US-11-170-653-31 US-10-984-376-8 US-11-170-653-31 US-10-984-376-8 US-11-170-653-31 US-10-793-626-184 US-11-170-653-33 US-10-793-626-184 US-11-170-653-33 US-10-793-626-184 US-11-170-653-33 US-10-793-626-184 US-11-170-653-33 US-10-793-626-184 US-11-170-653-33	0.000-110-01-00
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## ALIGNMENTS

Query Match 5.9%; Score 85; DB 6; Length 1565; Best Local Similarity 21.7%; Pred. No. 3.9; Matches 60; Conservative 37; Mismatches 96; Indels 84; Gaps .15;	2 NYKRFVVGVT-LSTFVFFLSDGAFSDANFSEGRRGLYIGSQY-KVGIPNFSNFSAEETIP   :	09	61	120	Db 109 PHKAWSASNLGRLEDYNMARFNKFVT	QY 180 MCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVEIAYH 239		Qy 240 PTALSDVPRTTSASATLATDYFGWEIGF 267
	6; Length 1565; 96; Indels 84; Gaps	Duery Match  5.9%; Score 85; DB 6; Length 1565;  Sest Local Similarity 21.7%; Pred. No. 3.9;  Matches 60; Conservative 37; Mismatches 96; Indels 84; Gaps  ANYKRFVVGVT-LSTFVFFLSDGAFSDANFSEGRRGLYIGSQY-KVGIPNFSNFSAEETIP	Duery Match  5.9%; Score 85; DB 6; Length 1565;  Sest Local Similarity 21.7%; Pred. No. 3.9;  Matches 60; Conservative 37; Mismatches 96; Indels 84; Gaps  2 NYKRFVVGVT-LSTFVFFLSDGAFSDANFSEGRRGLYIGSQY-KVGIPNFSNFSAEETIP  2 NYKRFVVGATDLSV	Duery Match  5.94; Score 85; DB 6; Length 1565;  Sest Local Similarity 21.74; Pred. No. 3.9;  Matches 60; Conservative 37; Mismatches 96; Indels 84; Gaps  2 NYKRFVVGVT-LSTFVFFLSDGAFSDANFSEGRRGLYIGSQY-KVGIPNFSNFSAEFTIP	Duery Match Best Local Similarity 21.7%; Pred. No. 3.9;  Matches 60; Conservative 37; Mismatches 96; Indels 84; Gaps  2 NYKRFVVGVT-LSTFVFFLSDGAFSDANFSEGRRGLYIGSQY-KVGIPNFSNFSAETIP	Duery Match  5.94; Score 85; DB 6; Length 1565;  Sest Local Similarity 21.74; Pred. No. 3.9;  Matches 60; Conservative 37; Mismatches 96; Indels 84; Gaps  2 NYKRFVUGVT-LSTFVFFLSDGAFSDANFSEGRRGLYIGSQY-KVGIPNFSNFSAETIP	Duery Match  5.9%; Score 85; DB 6; Length 1565;  Sest Local Similarity 21.7%; Pred. No. 3.9;  Matches 60; Conservative 37; Mismatches 96; Indels 84; Gaps  2 NYKREVVGVT-LSTFVFFLSDGAFSDANFSEGRRGLYIGSQY-KVGIPNFSNFSAETIP	Duery Match  5.94; Score 85; DB 6; Length 1565;  Sest Local Similarity 21.74; Pred. No. 3.9;  Autches 60; Conservative 37; Mismatches 96; Indels 84; Gaps  2 NYKRFVUGYT_LSTFVFFLSDGAFSDANFSEGRRGLYIGSQY-KVGIPNFSNFSAETIP

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ORGANISM: Homo sapiens
GENERAL INFORMATION:
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US-11-077-550-128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 TLSTFVFFLSDG--AFSDANFSEGRRGLYIGSQYKVGIP--NFSNFSAEE----TIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TPEEIVKFIKDENVEFVDVRFTD----LPGTEQHFSIPAASFDADTIEEGLAFDGSSIR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GITKKIFALGLDKSEIN-----SYDP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 KAEQYLASTGIADTCNFGAEAEFYLFDSVRYSTEMNSGFYEVDTEEGWWNRGKE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 98
                                                                                                                                                                                                                                               APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
TITLE OF INVENTION: METABACIERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION NUMBER: 05/606,740
PRIOR FILING DATE: 1909-06-23
PRIOR FILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 GISLPKFSYQVKFG---VNYPLNVNTML 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Corynebacterium glutamicum US-11-055-822-98
                                                                                                   Sequence 98, Application US/11055822 Publication No. US20050260707A1 GENERAL INFORMATION:
APPLICANT: Pompejus, Markus APPLICANT: Kroger, Burkhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      원
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US-11-094-519A-40; Sequence 40, Application US/11094519A; Publication No. US20050281810A1

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82 TRSYDPTYASSFAGFSGIIGYYVNDFRVEFEGSYENFEPERQWY-----PENSQ-SYKFF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641 KVŠWLPPPSGTQNGF--ITGYKIRHRKTTRRGEMETLEPNNLWYLFTGLEKGSQYSFQVS 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 -----GVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVEI 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.8%; Score 83.5; DB 7; Length 14 Best Local Similarity 20.5%; Pred. No. 4.8; Matches 54; Conservative 40; Mismatches 104; Indels
APPLICANT: LEVINE, ZUTITION OF INTERNATIVE SPLICING FILE REFERENCE: 2786-0140P CURRENT APPLICATION UNRERS. US/11/094,519A CURRENT APPLICATION NUMBER: US/09/695,293 PRIOR APPLICATION NUMBER: US/09/695,293 PRIOR PELING DATE: 2005-03-31 PRIOR PELING DATE: 2000-10-25 PRIOR PELING DATE: 1999-10-25 NUMBER OF SEQ ID NOS: 52 SOFTWARE: Patentin Ver. 2.1 SEG ID NO 40 LENGTH: 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 GSQYKV-GIPNFSNFSAEETI----PGI-TKKIFALGLD---
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APPLICANT: Stancombe, Patrick
APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130004
CURRENT APPLICATION NUMBER: US/11/077,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 10/241,550
PRIOR APPLICATION NUMBER: 10/241,596
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: 00/255,829
PRIOR PLILING DATE: 1999-02-23
PRIOR FILING DATE: 1997-08-22
PRIOR PLILING DATE: 1997-08-22
PRIOR PLILING DATE: 1997-08-22
PRIOR PLILING DATE: 1996-12-27
PRIOR APPLICATION NUMBER: 08/782,893
PRIOR PLILING DATE: 1996-12-27
PRIOR PLILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1006-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shone, Clifford Charles APPLICANT: Quinn, Conrad Padraig APPLICANT: Foster, Keith Alan APPLICANT: Chaddock, John APPLICANT: Marks, Philip
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                5 RFVVGVTLSTFVFFLSDGAFSDANF-----SEGRRGLYIGSQYKVGIPNFSNFSAE 55
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                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                  Query Match 5.6%; Score 81; DB 7; Length 876; Best Local Similarity 20.4%; Pred. No. 4.4; Matches 68; Conservative 39; Mismatches 100; Indels 126;
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US-LILUV/-DSD-LIZE

PUBLICATION NO. US20050244435A1

GENERAL INFORMATION:

APPLICANT: Shone, Clifford Charles

APPLICANT: Quinn, Conrad Padraig

APPLICANT: Guinn, Conrad Padraig

APPLICANT: Chaddock, John

APPLICANT: Chaddock, John

APPLICANT: Statcon, J. Mark

APPLICANT: Statcon, J. Mark

APPLICANT: Statcon, J. Mark

APPLICANT: Statcon, J. Mark

APPLICANT: Statcon, J. Mark

APPLICANT: Statcon, J. Mark

APPLICANT: Rayne, John

TILLE OF INVARTION: Recombinant Toxin Fragments

FILE REFERENCE: 1581.0130004

CURRENT APPLICATION NUMBER: 10/241,596

PRIOR FILING DATE: 1999-02-23

PRIOR FILING DATE: 1999-02-23

PRIOR FILING DATE: 1996-12-13

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                                                                                                                          TYPE: PRT / ORGANISM: Clostridium botulinum US-11-077-550-128
NUMBER OF SEQ ID NOS: 179
SOFTWARE: Patentin version 3.1
SEQ ID NO 128
LENCTH: 876
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; ORGANISM: Clos
US-11-077-550-126
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                                                                                                                     5 REVVGVILSTEVEFLSDGAFSDANF-----SEGRRGLYIGSQYKVGIPNFSNFSAE 55
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Query Match

5.6%; Score 81; DB 7; Length 877;

Best Local Similarity 20.4%; Pred. No. 4.4;

Matches 68; Conservative 39; Mismatches 100; Indels 126;
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APPLICANT: Stateonbe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Wayne, Jonathan
TITLE GOT INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130004
CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
PRIOR PILING DATE: 2005-09-12
PRIOR APPLICATION NUMBER: US/225,829
PRIOR FILING DATE: 1999-02-23
PRIOR PILING DATE: 1999-02-23
PRIOR PELLORYION NUMBER: 09/782,893
PRIOR PELLORYION NUMBER: 08/782,893
PRIOR PELLOR DATE: 1996-12-27
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR PILING DATE: 1996-10-13
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR PILING DATE: 1996-10-13
PRIOR PILING DATE: 1996-10-13
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Publication No. US20050244435A1
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quim, Conrad Padraig
APPLICANT: Foster, Keith Alan
APPLICANT: Chaddock, John
APPLICANT: Marks, Philip
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Best Local Similarity 20.4%
Matches 68; Conservative
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us-10-731-554-46.rapbn

DD 322 ITTANPSSPNKIGEYKOKLIRKYRFVVESSGEVTVNRRVEVELYNELTGIFTERPNYAK- 380  QY 141 ATMSDNKFTVLENNGVUDKSLAVNVCYDIASGSIPLAPYMCAGVGADYIRKLGISLEK 198  B381 ITANGNNKFTVLENNGVUDKSLAVNVCYDIASGSIPLAPYMCAGVGADYIRKLGISLEK 198	APPLICATION NUMBER: 08/782,893 APPLICATION NUMBER: 1996-12-27 APPLICATION NUMBER: GB9625996.5 FILING DATE: 1996-12-13 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-08-23 FILING DATE: 1996-1996-1996-1996-1996-1996-1996-1996	MALCHES 68; CORRETACLIVE 59; MISMACCHES 100; INGLES 128; Caps 10;  Qy 5 RFVVGVILSTPVPFLSDGAFSDANFSEGRRGLYIGSQYKVGIPNFSNE 55
DD 208 REW-LLTYSNATNDVGBGRFSKSEFCMDPILILMHELNHAMHNLYGIAIPND 257  S	CURRENT FILING DATE: 2005-03-11 PRIOR APPLICATION NUMBER: 10/241,596 PRIOR FILING DATE: 2002-00-12 PRIOR FILING DATE: 2002-00-12 PRIOR FILING DATE: 1999-02-23 PRIOR FILING DATE: 1999-02-23 PRIOR FILING DATE: 1997-08-22 PRIOR FILING DATE: 1997-08-22 PRIOR PILING DATE: 1996-12-27 PRIOR PILING DATE: 1996-12-13 PRIOR APPLICATION NUMBER: GB9625996.5 PRIOR PILING DATE: 1996-12-13 PRIOR APPLICATION NUMBER: GB9617671.4 PRIOR PILING DATE: 1996-08-23 PRIOR PILING DATE: 1996-08-33 NUMBER OF SEQ ID NOS: 179 SOFTWARE: Patentin version 3.1 SEQ ID NO 124	о <u>хахах</u>

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RESULT 11
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262 QTISSVTSNIFYSQYNVKLEYAEIYAFGGPTIDLIPKSARKYFBEKALDYYRSIAKRLNS 321
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                                           419 SNLNVLFMGQNLSRNPALRKVNPENMLYLFTKFCHKAIDGRSLYNKTLDCRELLVKNTDL 478
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PSYQVKP-GVNY-----PLNVNTMLF------GGGYYHKVVG---
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                                                                                                                                                                                                                                                                                                                                          Sequence 116, Application US/11077550

Publication No. US20050244435A1
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Oninn, Conrad Padraig
APPLICANT: Oninn, Conrad Padraig
APPLICANT: Foster, Keith Alan
APPLICANT: Foster, Keith Alan
APPLICANT: Stancombe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Marks, Philip
CURRENT MARS, DONATHAN
APPLICANT: WARNE, US, 10/241, 596
FRICH REFRERNCE: 1581.013004
CURRENT FILING DATE: 2005-09-12
FRICH APPLICATION NUMBER: 09/255, 829
FRICH FILING DATE: 1999-02-23
FRICH FILING DATE: 1999-02-23
FRICH FILING DATE: 1999-02-23
FRICH FILING DATE: 1999-02-23
FRICH FILING DATE: 1999-02-23
FRICH FILING DATE: 1996-12-37
FRICH FILING DATE: 1996-12-37
FRICH FILING DATE: 1996-12-37
FRICH APPLICATION NUMBER: GB9655996.5
FRICH FILING DATE: 1996-12-37
FRICH APPLICATION NUMBER: GB965996.5
FRICH FILING DATE: 1996-12-37
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FRICH FILING DATE: 1996-12-37
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FRICH APPLICATION NUMBER: GB965996.5
FRICH APPLICATION NUMBER: GB965996.5
FRICH APPLICATION NUMBER: GB967971.4
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                                                                                                                                ------ DRHERVEIAYHPTALS 244
                                                                                                                                                                     | : | : | : | : | 479 PFIGDISDVKTDIFLRKDINEETEVIYYPDNVS 511
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Best Local Similarity 20.4%
Matches 68; Conservative
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LENGTH: 912
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322 ITTANPSSFNKYIGEYKOKLIRKYRFVVESSGEVTVNRNKFVELYNELTQIFTEFNYAK- 380
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262 QTISSVTSNIFYSQYNVKLEYAEIYAFGGPTIDLIPKSARKYFEEKALDYYRSIAKRLNS 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   881 IYNVQNRKIYLSNVYTPVTANILDDNV-YDIQN--------GFNIPK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 FSYQVKF-GVNY-----PLINVNTMLF-------GGGYYHKVVG------ 228
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                                                                                                                                                                                                                                 APPLICANT: Chaddock, John
APPLICANT: Chaddock, John
APPLICANT: Chaddock, John
APPLICANT: Chaddock, John
APPLICANT: Sutton, J. Mark
APPLICANT: Statonowe, Patrick
APPLICANT: Statonowe, Patrick
APPLICANT: Rayne, Jonathan
TITLB OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130004
CURRENT FILING DATE: 2002-09-12
PRIOR PRILOR DATE: 2002-09-12
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1996-12-13
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                                                                                                              APPLICANT: Shone, Clifford Charles APPLICANT: Quinn, Conrad Padraig APPLICANT: Foster, Keith Alan APPLICANT: Chaddock, John APPLICANT: Marks, Philip APPLICANT: Sutton, J. Mark APPLICANT: Stancombe, Patrick
Application US/11077550
5. US20050244435A1
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        ; Sequence 120, Applic; Publication No. US20; GENERAL INFORMATION:
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US-11-170-653-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 RFVVGVTLSTFVFFLSDGAFSDANF-----SEGRRGLYIGSQYKVGIPNFSNPSAE
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Best Local Similarity 20.4%; Pred. No. 4.8;
Matches 68; Conservative 39; Mismatches 100; Indels 126; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 IYNVQNRKIYLSNVYTPVTANILDDNV-YDIQN------
                                                                                                          APPLICANT: Chaddock, John
APPLICANT: Chaddock, John
APPLICANT: Chaddock, John
APPLICANT: Sutton, J. Mark
APPLICANT: Statcombe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130004
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 10/241,596
PRIOR APPLICATION NUMBER: 09/255,829
PRIOR APPLICATION NUMBER: 09/255,829
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1996-12-27
PRIOR PELICATION NUMBER: GB9625996.5
PRIOR FILING DATE: 1996-12-27
PRIOR PELICATION NUMBER: GB9617671.4
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 179
SOFTWARE: Patentin version 3.1
SEQ ID NO 122
LENGTH: 944
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Publication No. US20050244435A1
GENERAL INFORMATION:
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APPLICANT: Ouinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
APPLICANT: Chaddock, John
APPLICANT: Sutton, J. Mark
APPLICANT: Sutton, J. Mark
APPLICANT: Stancombe, Patrick
Shone, Clifford Charles
Quinn, Conrad Padraig
Foster, Keith Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Clostridium botulinum US-11-077-550-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-077-550-118
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Sequence 29, Application US/11170653
Publication No. US20050271769A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sibbesen, Ole
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
CURRENT APPLICATION NUMBER: US/11/170,653
CURRENT PILING DATE: 2005-06-23
FRIOR APPLICATION NUMBER: US/10/237,386
FRIOR APPLICATION NUMBER: PCT/IB01/00426
FRIOR FILING DATE: 2001-03-08
FRIOR FILING DATE: 2000-03-08
FRIOR FILING DATE: 2000-03-08
FRIOR FILING DATE: 2000-03-08
FRIOR APPLICATION NUMBER: GB 0015751.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 ETIPGITKKIF----ALGLDKSEINTHSNFTRSYDPTYASSF-----
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TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130004
CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 10/241,596
PRIOR APPLICATION NUMBER: 09/25,829
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR PLING DATE: 1996-12-7
PRIOR PLING DATE: 1996-12-7
PRIOR PLING DATE: 1996-12-7
PRIOR PLING DATE: 1996-12-7
PRIOR PLING DATE: 1996-12-7
PRIOR PLING DATE: 1996-12-7
PRIOR PLING DATE: 1996-12-13
PRIOR PLING DATE: 1996-10-13
PRIOR PLING DATE: 1996-10-13
PRIOR PLING DATE: 1996-08-23
NUMBER OF SEQ ID NOWS: 179
NUMBER OF SEQ ID NOS: 179
NUMBER OF SEQ ID NOS: 179
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SEQ ID NO 118
LENGTH: 950
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SEQ ID NO 3
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                                                                                                                                                                                                  DB 7; Length 219;
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APPLICANT: Xu, Siqun
TITLE OF INVENTION: NEMATODE PAN AND ZP RECEPTOR-LIKE
TITLE OF INVENTION: SEQUENCES
FILE REFERENCE: 12557-015001
CURRENT APPLICATION NUMBER: US/11/191,374
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: US/10/771,708
PRIOR APPLICATION NUMBER: US 60/444,771
PRIOR FILING DATE: 2003-02-04
PRIOR FILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 54
SOPTWARE: FastESQ for Windows Version 4.0
SEQ ID NO 3
LENGTH....
                                                                                                                                                                                                    ch 5.4%; Score 78; DB 7
1 Similarity 20.5%; Pred. No. 1.3;
43; Conservative 32; Mismatches
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Publication No. US20050260673A1
GENERAL INFORMATION:
APPLICANT: Hreeko, Michelle Coutu
APPLICANT: Milams, Derryck J.
APPLICANT: Williams, Derryck J.
APPLICANT: Chiapelli, Brandi
APPLICANT: Chiapelli, Brandi
APPLICANT: Bablitc, Catherine
APPLICANT: Bablitc, Catherine
APPLICANT: Morek, Andrew P.
APPLICANT: Malay Andrew P.
APPLICANT: Bavila-Aponte, Jennifer A.
APPLICANT: Bavila-Aponte, Jennifer A.
APPLICANT: Bradley, John D.
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PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 29
                                                                                       ; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
US-11-170-653-29
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Best Local Similarity
Matches 43; Conserv
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118 FEPEROWYPENSQSYKFFALSR-NATNSDNKFIVLENNGVVDKSLNVNVCYDIASGSIPL 176
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TITLE OF INVENTION: NEWATODE PAN AND ZP RECEPTOR-LIKE
TITLE OF INVENTION: SEQUENCES
TITLE OF INVENTION: SEQUENCES
CURRENT PRILING DATE: 12557-015001
CURRENT PILING DATE: 2005-07-28
PRIOR PILING DATE: 2004-02-04
PRIOR FILING DATE: 2004-02-04
PRIOR FILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTERQ for Windows Version 4.0
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Job time : 19 secs
                                                                                                                                                                                                                                      APPLICANT: Hresko, Michelle Coutu
APPLICANT: McLaird, Merry B.
APPLICANT: Williams, Deryck J.
APPLICANT: Williams, Deryck J.
APPLICANT: Chiapelli, Brandi
APPLICANT: Baublite, Catherine
APPLICANT: Kloek, Andrew P.
APPLICANT: Nioek, Andrew P.
APPLICANT: Brandia-Aponce, Jennifer A.
APPLICANT: Brandia-Aponce, Jennifer A.
APPLICANT: Brandia-Aponce, Jennifer A.
APPLICANT: Brandia-Aponce, Jennifer A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Strongyloides stercoralis
US-11-191-375-3
                                                                                                                                                                       Sequence 3, Application US/11191375; Publication No. US20050260674A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 36; Conservative
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APPLICANT:
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APPLICANT:
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December 28, 2005, 15:38:05; Search time 79 Seconds (without alignments) 1433.313 Million cell updates/sec
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'cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-314-639-4	US-10-369-293-14	US-10-285-042-14	US-10-680-349-10	US-10-731-554-10	US-10-901-714-4	US-10-901-774-4	US-09-846-808-9	US-10-284-986-9	US-10-369-293-9	US-10-285-042-9	US-10-059-964-30	US-10-314-639-30	US-10-901-714-30	US-10-901-774-30	US-10-059-964-24	US-10-314-639-24	US-10-901-714-24	
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Sequence 46, Application US/09811007

Sequence 46, Application US/09811007

Publication No. US20030185849A1

GENERAL INFORMATION:

APPLICANT: Walker, David H.

APPLICANT: Walker, David H.

APPLICANT: Walker, David H.

APPLICANT: Walker, David H.

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APPLICANT: Walker, David H.

APPLICANT: Walker, David H.

APPLICANT: Walker, David H.

APPLICANT: Walker, David H.

TITLE OF INVENTION: Genes of Enrlichia canis and Uses Thereof

FILE REFERENCE: D6152CIP2

CURRENT APPLICATION NUMBER: US/09/811,007

CURRENT FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-09-12

NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ITKKIFALGLDKSEINTHSNFTRSYDPTYASSFAGFSGIIGYYVNDFRVEFEGSYENFEP
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Matches 271; Conservative
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ORGANISM: Ehrlichia canis
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Fublication No. US20030073095A1

GENERAL INFORMATION:

APPLICANT: Walker, David H.

APPLICANT: Walker, Jere W.

APPLICANT: Wue-Jie

TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein

TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof

TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein

TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof

TITLE OF INVENTION: HOMBER: US/10/662,051

CURRENT PRICATION NUMBER: US/09/660,587

FRIOR PELICATION NUMBER: US/09/660,587

FRIOR APPLICATION NUMBER: US/09/660,587

FRIOR FILING DATE: 2000-09-12

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 46

LENGTH: 271
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                                                           APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
APPLICANT: Walker, Jare W.
APPLICANT: Webride, Jare W.
APPLICANT: W. Xue-Jie
TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REPERENCE: D6152CIP2/D1
CURRENT APPLICATION NUMBER: US/10/062,624
FRIOR APPLICATION NUMBER: 09/660,587
PRIOR APPLICATION NUMBER: 09/660,587
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: amino acid sequence of E. canis p28-9 protein US-10-062-624-46
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Best Local Similarity 100.0%; Pred. No. 2.2e-134;
Matches 271; Conservative 0; Mismatches 0;
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Sequence 46, Application US/10062624 Publication No. US20020115840A1 GENERAL INFORMATION:
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ORGANISM: Ehrlichia canis
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181 CAGYGADYIKPLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVEIAYHP 240
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PUblication No. US20030096250A1
GENERAL INFORMATION.
APPLICANT: Walker, David H.
APPLICANT: W. Xue-Jie
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
TITLE OF INVENTION: UNMERR: US/10/062,920
CURRENT FILING DATE: 2002-01-31
FRIOR PAPLICATION NUMBER: US/09/660,587
FRIOR FILING DATE: 2000-09-12
FRIOR PELING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 46
IEBNGTH: 271
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         Length
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   100.0%; Score 1434; DB 4;
100.0%; Pred. No. 2.2e-134;
ive 0; Mismatches 0;
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Query Match
Best Local Similarity 100.
Matches 271; Conservative
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RESULT 7
US-09-846-808-20
SEQ ID NO 46
LENGTH: 271
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Publication No. US20040247616A1

GENERAL INFORMATION:

APPLICANT: Walker, David H.

APPLICANT: Walker, David H.

APPLICANT: Yu, Xue-Jie

TITLE OF INVENTION: Homelogous 28-kilodalton Immunodominant Protein

TITLE OF INVENTION: Homelogous 28-kilodalton Immunodominant Protein

TITLE OF INVENTION: Homelogous 28-kilodalton immunodominant Protein

TITLE OF INVENTION: OWNBER: US/10/731,554

CURRENT APPLICATION NUMBER: US/09/811,007

FRIOR APPLICATION NUMBER: 09/660,587

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-09-12

NUMBER OF SEQ ID NOS: 46
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APPLICANT: Walker:
APPLICANT: Walker:
APPLICANT: Yu. Xue-Jie
APPLICANT: Yu. Xue-Jie
APPLICANT: Yu. Xue-Jie
TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Bhrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2/D1
CURRENT APPLICATION NUMBER: US/10/680,349
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US/10/062,624
PRIOR APPLICATION NUMBER: 09/660,587
PRIOR APPLICATION NUMBER: 09/660,587
PRIOR FILING DATE: 2000-09-12
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Sequence 46, Application US/10680349
Publication No. US20040198951A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 271; Conservative
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LENGTH: 271
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| Sequence 20, Application US/09846808
| Patent No. US20020064531A1
| GENERAL INFORMATION:
| APPLICANT: Walker, David H. APPLICANT: Yu, Xu-Jie
| TITLE OF INVENTION: Ehrlichia chaffeensis 28 kDa Outer Membrane
| TITLE OF INVENTION: Protein Multigene Family
| FILE REFERENCE: D6311
| CURRENT PAPLICATION NUMBER: US/09/846,808
| CURRENT FILING DATE: 2001-05-01
| PRIOR FILING DATE: 2000-05-01
| WHORE OF SEQ ID NOS: 53
| SEQ ID NO 20
| LENGTH: 271
                                                                   ; FEATURE:
; OTHER INFORMATION: amino acid sequence of E. canis p28-9 protein
US-10-731-554-46
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                                                                                                                                                         100.0%; Score 1434; DB 5; 100.0%; Pred. No. 2.2e-134;
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Best Local Similarity 100.0
Matches 271; Conservative
LENGTH: 271
TYPE: PRT
ORGANISM: Ehrlichia canis
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Sequence 20. Application US/10285042

Publication No. US20030158383A1

GENERAL INPORMATION:
APPLICANT: Walker:
TITLE OF INVENTION: Ehrlichia chaffeensis 28 kDa Outer Membrane
TITLE OF INVENTION: Protein Multigene Family
FILE REFERENCE: D631102

CURRENT APPLICATION NUMBER: US/10/285,042

CURRENT APPLICATION NUMBER: 09/846,808

PRIOR PILING DATE: 2001-031

PRIOR FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 53
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    i. Score 1194; DB 4; Length 2
    i. Pred. No. 2e-110;
    33; Mismatches 25; Indels

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Best Local Similarity 78.6%; Pred. No. 2e-110;
Matches 213; Conservative 33; Mismatches 25; Indels
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                                                                                                                     of
                                                                                                                     Membrane Protein
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                                                                                                                  OTHER INFORMATION: P28-20 Outer Membrane OTHER INFORMATION: Ehrlichia chaffeensis
SEQ ID NO 20
LBNCTH: 271
TYPE: BT
ORGANISM: Ehrlichia chaffeensis
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Best Local Similarity 78.6%;
Matches 213; Conservative 3:
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US-10-285-042-20
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  CAGUGADY I KFLGISL PKFSYQVKFGVNY PLNVNTML FGGGYYHKVVGDRHERVBIAYHP
                           181 CAGVGADYIKFLGISLPKFSYQVKFGVNYPVSVNVMLFGGGYYHKVIGNRYERVEIAYHP
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; APPLICANT: Walker, David H.; APPLICANT: Walker, David H.; APPLICANT: Walker, David H.; TITLE OF INVENTION: Ehrlichia chaffeensis 28 kDa Outer Membrane; TITLE OF INVENTION: Protein Multigene Family; FILE REPERBURE: D6311D1; CURRENT APPLICATION NUMBER: US/10/284,986; CURRENT APPLICATION NUMBER: 0202-10-31; PRIOR FILING DATE: 2001-05-01; NUMBER OF SEQ ID NOS: 53
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Publication No. US20030147913A1

GENERAL INFORMATION:

APPLICANT: Walker, David H.

APPLICANT: Wu, Xu-Jie

TITLE OF INVENTION: Ehrlichia chaffeensis 28 kDa Outer Membrane

TITLE OF INVENTION: Protein Multigene Family

FILE REFERENCE: D6331D3

CURRENT APPLICATION NUMBER: US/10/169,293

CURRENT FILING DATE: 2003-02-18

PRIOR APPLICATION UNDERR: 09/846,808

PRIOR PILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 53
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OTHER INFORMATION: P28-20 Outer Membrane Protein of
OTHER INFORMATION: Ehrlichia chaffeensis
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                                                                                              241 TALSDVPRITSASATLNTDYFGWEIGFRFAL 271
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LENGTH: 271
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Publication No. US20020115840A1
GENERAL INPORMATION:
APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
TILLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
TILLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
TILLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
TILLE OF INVENTION: Genes of Bhrlichia canis and Uses Thereof
FILE REFERENCE: D612CIP2/D1
CURRENT APPLICATION NUMBER: 09/660,587
                                                                                                                                                                                                      Sequence 42, Application US/09811007
Publication No. US20030185849A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2
CURRENT APPLICATION NUMBER: US/09/811,007
CURRENT FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-09-12
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                                                                                             241 AILINVPKTISASATLDIDYFGWEVGMRFTL 271
                                                                          241 TALSDVPRTTSASATLNTDYFGWEIGFRFAL
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ORGANISM: Ehrlichia canis
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APPLICANT: Rikihisa, Yasuko
APPLICANT: Rikihisa, Yasuko
APPLICANT: Rikihisa, Vasuko
APPLICANT: Ohasi, No. US20020120115Alio
TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia canis and Ehrlichia
TITLE OF INVENTION: Chaffeensis
FILE REPERENCE: 22727/04021
CURRENT APPLICATION NUMBER: US/10/059,964
CURRENT FILING DATE: 2002-01-28
EARLIER APPLICATION NUMBER: 09/314,701
EARLIER FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
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177 YDITAEGVSFVPYACAGIGADLITIFKDLNL-KFAYQGKIGISYPITPEVSAFIGGYYHG 235
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Best Local Similarity 40.5%; Pred. No. 4.1e-42;
Matches 115; Conservative 50; Mismatches 98; Indels
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35.5%; Score 509.5; DB 4;
Best Local Similarity 40.5%; Pred. No. 4.1e-42;
Matches 115; Conservative 50; Mismatches 98;
                                                                                                                                                                                        , OTHER INFORMATION: amino acid sequence of US-10-062-624-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-059-964-48
US-10-059-964-48
; Sequence 48, Application US/10059964
; Publication No. US20020120115A1
; GENERAL INFORMATION:
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Ehrlichia canis
                                                                                                               TYPE: PRT
ORGANISM: Ehrlichia canis
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                         58 -IPG---ITKKIFALGLDKSEINTHSNFTR----SYDPTYASSFAGFSGIIGYYVNDFR 108
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                                                                                                                                                                                                                                  US-10-062-051-42

| Sequence 42, Application US/10062051
| Publication No US20030073095A1
| Publication No US20030073095A1
| GENERAL INFORMATION:
| APPLICANT: Walker, David H. |
| APPLICANT: William Webride, Jere W. |
| APPLICANT: William Webride, Jere W. |
| APPLICANT: Webride, Jere W. |
| APPLICANT: Webride, Jere W. |
| APPLICANT: Webride, Jere W. |
| APPLICANT: Webride, Jere W. |
| APPLICANT: Webride, Jere W. |
| APPLICANT: Webride, Jere W. |
| TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof FILE REFERENCE: D6152C1P2 |
| FILE REFERENCE: D6152C1P2 |
| FILE REFERENCE: D6152C1P2 |
| FRIOR PILING DATE: 2002-01-31 |
| PRIOR APPLICATION NUMBER: 09/261,358 |
| PRIOR APPLICATION NUMBER: 09/261,358 |
| PRIOR FILING DATE: 1999-03-03 |
| PRIOR FILING DATE: 1999-03-03 |
| PRIOR FILING DATE: 1999-03-03 |
| PRIOR FILING DATE: 1999-03-03 |
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Publication No. US20030096250A1
GENERAL INFORMATION No. US20030096250A1
GENERAL INFORMATION No. US20030096250A1
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xu-01e
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152C1P2
CURRENT APPLICATION NUMBER: US/10/062,920
CURRENT FILING DATE: 2002-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein US-10-062-051-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.5%; Score 509.5; DB 4; Length 280; 40.5%; Pred. No. 4.1e-42; tive 50; Mismatches 98; Indels 21
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Best Local Similarity 40.5%;
Matches 115; Conservative
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ORGANISM: Ehrlichia canis
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LENGTH: 280
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58 -IPG---ITKKIFALGLDKSEINTHSNFTR----SYDPTYASSFAGFSGIIGYYVNDFR 108
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                                                                                                                                                                                                                                                     OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                           35.5%; Score 509.5; DB 4; Length 280; 40.5%; Pred. No. 4.1e-42; ive 50; Mismatches 98; Indels 21
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PRIOR APPLICATION NUMBER: US/09/660,587
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 09/261,358
PRIOR FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 42
LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                            Matches 115; Conservative
                                                                                                                                                                               TYPE: PRT
ORGANISM: Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

using sw model OM protein - protein search, December 28, 2005, 13:52:57; Search time 90 Seconds (without alignments) 1323.018 Million cell updates/sec Run on:

US-10-731-554-46

1 MNYKRFVVGVTLSTFVFFLS......ASATLNTDYFGWEIGFRFAL 271 **BLOSUM62** Scoring table: Sequence:

Perfect score:

Gapop 10.0 , Gapext 0.5

2443163 segs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 21:\* 1: geneseqp198 Database :

geneeqp1980s:\* geneeqp1990s:\* geneeqp2000s:\* geneeqp2001s:\* geneeqp2003s:\* geneeqp2003bs:\* geneeqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:\*

					SUMMARIES		
Result No.	Score	* Query Match	Length	DB	ID	Description	
-	1434	100.0	271	5	AAU96118	Aau96118 Ehrlichia	ichia
1 (7)	1194	83.3	271	ហ	AAU73419	Aau73419 Ehrlichia	ichia
'n	509.5	35.5	280	'n	AAU96116	Aau96116 Ehrli	Ehrlichia
4	509.5	35.5	280	'n	ABG77958	Abg77958 Ehrli	Ehrlichia
ហ	509.5	35.5	280	9	ADA09781	-	canis
9	509.5	35.5	280	σ	ADW04274	_	Ehrlichia
7	507	35.4	283		AAY06944	Aay06944 E. ch	chafee
80	507	35.4			AAU96106		Ehrlichia
σ	507	35.4	283	ហ	AAU73413	Aau73413 Ehrlichia	ichia
10	507	35.4	283		ABG77936		ichia
11	507	35.4	283	9	ADA09737	ъ	chaffe
12	507	35.4	283	0	ADW04230	Adw04230 Erlichia	chia
13	494	34.4		8	AAY06957	Aay06957 E. ch	chafee
14	494	34.4		Ŋ	AAU73408	Aau73408 Ehrlichia	ichia
15	494	34.4	285	Ŋ	ABG77949	Abg77949 Ehrli	ichia
16	492			9	ADA09763	ы Ш	chaffe
17	492	34		6	ADW04256	Adw04256 Erlichia	chia
18	489		279	N	AAY06954	Aay06954 E. ch	chafee
19	489	34.1	279	Ŋ	ABG77946		Ehrlichia
20	489	34.1		9	ADA09757	м.	chaffe
21	489			0	ADW04250	Adw04250 Erlichia	chia
22	482	33.6		'n	AAU73405		Bhrlichia
23	463	32.3	283	8	AAY06955	Aay06955 E. ch	chafee
24	463	32.3	283	ß	AAU73406	Aau73406 Ehrli	Ehrlichia

E. chaffe	Erlichia	Ehrlichia	Ehrlichia	E. chaffe	Erlichia	Ehrlichia	E. canis	Ehrlichia	Ehrlichia	Ehrlichia	Ehrlichia	E. chaffe	Erlichia	E. canis	Ehrlichia	Ehrlichia	E. canis	Ehrlichia	E. canis	Ehrlichia
Ada09759	Adw04252	Aau73410	Abg77960	Ada09785	Adw04278	Abg77963	Ada09791	Adw04284	Abg77947	Aau73411	Abg77943	Ada09751	Adw04244	Aay06965	Aau96115	Abg77956	Aay06959	Abg77950	Ada09765	Adw04258
ADA09759	ADW04252	AAU73410	ABG77960	ADA09785	ADW04278	ABG77963	ADA09791	ADW04284	ABG77947	AAU73411	ABG77943	ADA09751	ADW04244	AAY06965	AAU96115	ABG77956	AAY06959	ABG77950	ADA09765	ADW04258
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283	283	298	298	298	298	281	281	281	283	300	291	291	291	293	293	293	288	288	288	288
32.3	32.3	31.8	31.8	31.8	31.8	31.7	31.7	31.7	31.7	31.2	30.7	30.7	30.7	30.5	30.5	30.5	30.4	30.4	30.4	30.4
463	463	455.5	455.5	455.5	455.5	455	455	455	455	447.5	440	440	440	437	437	437	435.5	435.5	435.5	435.5
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Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial. New recombinant homologous 28 kilodalton immunodominant protein from Ehrlichia canis, useful for treating Ehrlichia canis infections. AAU96118 standard; protein; 271 AA Yu X, Mcbride JW; 12-SEP-2001; 2001WO-US028759. 12-SEP-2000; 2000US-00660587. (first entry) Ehrlichia canis p28-9. (RERE-) RES DEV FOUND WPI; 2002-351882/38. N-PSDB; ABK68878 Ehrlichia canis. WO200222782-A2. 02-JUL-2002 21-MAR-2002. Walker DH, AAU96118; RESULT 1 AAU96118 

The invention relates to a recombinant homologous 28 kDa immunodominant protein, P28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably dispersed in a pharmaceutically acceptable carrier, is useful for inhibiting B. canis infection in a subject. (I) is useful in the development of vaccines and serodiagnostics that are particularly effective for disease prevention and serodiagnosis. AAU96100-AAU96118 represent the 28-kDa antigen amino acid sequences of the invention Claim 16; Fig 16; 106pp; English.

Sequence 271 AA;

Gaps ö Query Match 100.0%; Score 1434; DB 5; Length 271; Best Local Similarity 100.0%; Pred. No. 9.3e-145; Matches 271; Conservative 0; Mismatches 0; Indels 0;

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240 240

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109 VEFEGSYENFEPER--QWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVC 166
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                                                                                                                                                                                                                                                                                                                                                   Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
                                                       ERQWYPEGGESHKFPALSRESTVQDNKFIVLENDGVIDKSLNVNFCYDIAHGSIPLAPYM
                                                                                                           181 CAGVGADYIKFLGISLPKFSYQVKFGVNYPVSVNVMLFGGGYYHKVIGNRYERVEIAYHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVEIAYHP
ERQWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVCYDIASGSIPLAPYM
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Pred. No. 1.4e-45;
50; Mismatches 98;
                                                                                                                                               271
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                                                                                                                                                241 TALSDVPRTTSASATLNTDYFGWEIGFRFAL
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Best Local Similarity 40.5%;
Matches 115; Conservative 5
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                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins (P28-1 to P28-21) of Ehrlichiā chaffeensis. P28 proteins are encoded by a 28kDa outer membrane protein multigene family. P28 proteins are useful as a vaccine against E.chaffeensis. DNA encoding P28 is useful for transfecting a host cell. A&U73420 represent Ehrlichia chaffeensis P28 outer membrane proteins of the invention
                                                                  120
                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ITKKIFALGLDKSEINTHSNFTRSYDPTYASSFAGFSGIIGYYVNDFRVEFEGSYENFEP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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            ERQWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVCYDIASGSIPLAPYM
                                                                                                                                                                                          CAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVEIAYHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ehrlichia chaffeensis 28-kDa outer membrane protein, designated
l as a vaccine against Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERQWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVCYDIASGSIPLAPYM
                                                                                                                                                                         CAGUGADYIKPLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHKVVGDRHERVBIAYHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNYKRFVVGVTLSTFVFFLSDGAFSDANFSEGRRGLYIGSQYKVGIPNFSNFSAEETIPG
                                                                  ITKKIFALGLDKSEINTHSNFTRSYDPTYASSFAGFSGIIGYYVNDFRVEFEGSYENFEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to isolated and purified 28-kDa outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.3%; Score 1194; DB 5; Length 271; 78.6%; Pred. No. 5.2e-119; ive 33; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia; outer membrane protein; P28; antibiotic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                      protein P28-20.
                                                                                                                                                                                                                               TALSDVPRTTSASATLNTDYFGWEIGFRFAL 271
                                                                                                                                                                                                                                             TALSDVPRTTSASATLNTDYFGWEIGFRFAL 271
                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chaffeensis outer membrane
                                                                                                                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                                                                                                                       AAU73419 standard; protein; 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Fig 2; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000; 2000US-0201035P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2001; 2001WO-US013997
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEV FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-066527/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 271 AA
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Best Local Simi
Matches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2001
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                                                                                          61
                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RERE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walker
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The invention relates to an isolated polynucleotide encoding a variant of the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer membrane protein of E. canis, or an antigenic fragment of the E. canis P30 protein, or comprising a sequence which is the complement of nucleotide 99 through nucleotide 672 of ADA09764. Also disclosed are E. canis and E. chaffeensis outer membrane proteins and their encoding nucleic acids. The polynucleotides are useful for producing E. canis or E. chaffeensis outer membrane protein, for designing hybridisation probes for isolating and identifying cDNA and genomic clones encoding the OMP) or its allelic forms, for designing primers for PCR. The polypeptides encoded by the polynucleotide is useful for diagnosing human ehrlichiosis (Rocky mountain spotted fever) or canine ehrlichiosis. The present sequence represents an E. canis outer membrane protein.
                                            YDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHK 225
                                                             outer membrane protein, circulating leukocyte, monocytic ehrlichiosis;
Rocky Mountian spotted fever; canine ehrlichiosis; antigen.
1 MNYKRFVVGVTLSTFVFFLSDGAFSD---ANFSEGRRGLYIGSQYKVGIPNFSNFSAEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide encoding outer membrane protein P30 o
Bhrlichia canis or its variant or fragment, useful for producing
Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins
diagnosing and treatling ehrlichiosis.
                                                                                                                          VVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 509.5; DB 6
; Pred. No. 1.4e-45;
50; Mismatches 98
                                                                                                                                                                                                                                                                                                       canis outer membrane protein P30-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 30; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OHIS ) UNIV OHIO STATE RES FOUND
                                                                                                                                                                                                               ADA09781 standard; protein; 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.5%;
40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00314701.
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                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-553952/52.
N-PSDB; ADA09780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 280 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                 US6544517-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rikihisa Y,
                                                                                                                                                                                                                                                                           06-NOV-2003
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Best Local S
                                                                                                                                                                                                                                               ADA09781;
                                               167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used in the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the serum sample and the polypeptide, where formation of a complex is indicative of infection with E. chaffeenis. This sequence represents an Ehrlichia outer membrane protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 -IPG---ITKKIFALGLDKSEINTHSNFTR----SYDPTYASSFAGFSGIIGYYVNDFR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 VEFEGSYENFEPER--QWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVC 166
                                                                  YDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein of E.canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNYKRFVVGVTLSTFVFFLSDGAFSD---ANFSEGRRGLYIGSQYKVGIPNFSNFSAEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 280;
                                                                                                                                                                                                                                                                                                                                        Outer membrane protein; OMP; P30F; ehrlichiosis; infection.
                                                                                                                            Indels
                                                                                                            VVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outer membrane of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 509.5; DB 5;
Pred. No. 1.4e-45;
0; Mismatches 98;
                                                                                                                                                                                                                                                                                                           Bhrlichia canis outer membrane protein (P30F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             solated polynucleotide encoding an chaffeensis used in the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Fig 30B; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                  ABG77958 standard; protein; 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2002; 2002US-00059964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00314701
                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 40.5
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rikihisa Y, Ohashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-618954/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RIKI/) RIKIHISA Y. (OHAS/) OHASHI N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABS63299
                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                    US2002120115-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1999;
                                                                                                                                                                                                                                                                              15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Invention
                                                                                                                                                                                                                                                  ABG77958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated
                      117
                                                                                                            226
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Length 280;

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19-SEP-1997;
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05-JUL-1999
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                                                                                                                                                                 226
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Matches
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AAY06944
ID AAY0
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                                                                      YDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHK 225
-IPG---ITKKIFALGLDKSEINTHSNFTR-----SYDPTYASSFAGFSGIIGYYVNDFR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to nucleic acid sequences encoding outer membrane proteins (OMP) of Erlichia chaffeensis (designated as OMP proteins) and Ehrlichia canis (designated as P30F proteins). The OMP polymucleotide is useful in preparing a composition for diagnosing, treating or preventing an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present sequence is the Erlichia canis P30F protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehrlichia
                                                                                                                                                                                                                                                 purification; diagnosis; outer membrane protein; OMP; P30F protein;
           VEFEGSYENFEPER - - QWYPENSQSYKFFALSRNATNSDNKFIVLENNGVVDKSLNVNVC
                                               New polynucleotide encoding an outer membrane protein (OMP) of Ehrlich canis or Ehrlichia chaffeensis, useful in preparing a composition for diagnosing or preventing E. canis or E. chaffeensis infection.
                                                                                                                                                                                                                                                                                                                                /note= "Erlichia canis mature OMP protein"
                                                                                                           VVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                    Ehrlichia canis outer membrane protein (P30F), P30-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; SEQ ID NO 48; 122pp; English.
                                                                                                                                                                                                                                                                                                       1. .25
/label= Signal_peptide
                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                          ADW04274 standard; protein; 280
                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1998; 98US-0100843P.
19-MAY-1999; 99US-00314701.
28-JAN-2002; 2002US-00059964.
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                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-064871/07.
N-PSDB; ADW04273.
                                                                                                                                                                                                                                                 DNA purification; d infection; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKIHISA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OHASHI N.
                                                                                                                                                                                                                                                                           Ehrlichia canis.
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                                                                                                                                                                                                                                                                                                                                                   US2004265334-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rikihisa Y,
                                                                                                                                                                                                            24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                      30-DEC-2004
                                                                                                                                                                                            ADW04274;
28
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                                                                                                                                                                                                                                                                                               Key
Peptide
                                                                                                                                                                                                                                                                                                                         Protein
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Length 280;

Score 509.5; DB 9 Pred. No. 1.4e-45;

35.5%; 40.5%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                  225
                                                                                                                                                                                                                                                                                                                                                                                 The invention provides isolated outer membrane proteins (OMP) from Barlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the CMP family and consist of proteins CMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs. (Updated on 27-AUG-2003 to correct OS fleid.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia
                                                                                                                                                                                                                                                                            YDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGGYYHK
                                                                                - IPG---ITKKIFALGLDKSEINTHSNFTR----SYDPTYASSFAGFSGIIGYYVNDFR
                                                                                                                                                                                               61 PINGTNSLTKKVFGLKKD-GDITKKDDFTRVAPGIDFQNNLIS---GFSGSIGYSMDGPR
                                                                                                                                                                                                                                                109 VEFEGSYENFEPER -- OWYPENSQSYKFFALSRNATUSDNKFIVLENNGVVDKSLNVNVC
                                                 MNYKRFVVGVTLSTFVFFLSDGAFSD - - - ANFSEGRRGLYIGSQYKVGI PNFSNFSAEET
Gaps
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel outer membrane proteins from Ehrlichia chaffeensis and canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           canis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane protein, \mathsf{OMP}_i Ehrlichia chafeensis, E. detection, \mathsf{dog}.
  98;
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY06944 standard; protein; 283
  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. chafeensis OMP-1B protein.
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Matches 116; Conservative
  115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OHIS ) UNIV OHIO STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rikihisa Y, Ohashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ehrlichia chaffeensis.
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The invention relates to isolated and purified 28-kDa outer membrane proteins (P28-1 to P28-21) of Ehrlichia chaffeensis. P28 proteins are encoded by a 28kDa outer membrane protein multighene family. P28 proteins are useful as a vaccine against E.chaffeensis. DNA encoding P28 is useful for transfecting a host cell. ABUT3400-AAUT3420 represent Ehrlichia chaffeensis P28 outer membrane proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 RVEFEGSYENFEPERQWYPENSQS-----YKFFALSRNATNSDNKFIVLENNGVVDKSLN 162
                             VNVCYDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGG 221
        EET-IPG---ITKKIFALGLDKSEINTHSNFTRSYDPTYA---SSFAGFSGIIGYYVNDF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel Ehrlichia chaffeensis 28-kDa outer membrane protein, designated useful as a vaccine against Ehrlichia chaffeensis.
                                                                                                                                                           1 MNYKRFVVGVTLSTFVFFLSDGAF----SDANFSEGRRGLYIGSQYKVGIPNFSNFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 EET-IPG---ITKKIFALGLDKSEINTHSNFTRSYDPTYA---SSFAGFSGIIGYYVNDF
                                                                       26:
                                                                                                                                                                                                          YYHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bhrlichia; outer membrane protein; P28; antibiotic; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 283;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          membrane protein P28-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100;
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40.3%; Pred. No. 2.7e-45;
tive 46; Mismatches 100;
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                                                                                                                                                                                                                                                                                                                            AAU73413 standard; protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2001; 2001WO-US013997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000; 2000US-0201035P
                                                                                                                                                                                                                                                                                                                                                                                                                            Bhrlichia chaffeensis outer
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 40.3
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEV FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200183699-A2
                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RERE-) RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Walker DH,
                                                                                                                                                                                                                                                                                                                                                             AAU73413;
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                                                                                                                                            163
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             55
                                                                             108
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                                                                                                                                                                                                                EET-IPG---ITKKIFALGLDKSEINTHSNFTRSYDPTYA---SSFAGFSGIIGYYVNDF 107
                                                                                                                            108 RVEPEGSYENFEPERQWYPENSQS-----YKFFALSRNATNSDNKFIVLENNGVVDKSLN 162
                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a recombinant homologous 28 kDa immunodominant protein, P28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably dispersed in a pharmaceutically acceptable carrier, is useful for inhibiting B. canis infection in a subject. (I) is useful in the development of vaccines and serodiagnostics that are particularly effective for disease prevention and serodiagnosis. AAUS6100-AAU96118 represent the 28-kDa antigen amino acid sequences of the invention. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNYKRFVVGVTLSTFVFFLSDGAF----SDANFSEGRRGLYIGSQYKVGIPNFSAFSA
                  VNVCYDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGG
MNYKRFVVGVTLSTFVFFLSDGAF-----SDANFSEGRRGLYIGSQYKVGIPNFSNFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant homologous 28 kilodalton immunodominant protein from Ehrlichia canis, useful for treating Ehrlichia canis infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                               YYHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                                                                                                                                                                                 Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 507; DB 5; Length 28;
; Pred. No. 2.7e-45;
46; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 3; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                 AAU96106 standard; protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcbride JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2001; 2001WO-US028759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.3%;
Matches 116; Conservative 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrlichia chafeensis OMP-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrlichia chaffeensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 283 AA;
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02-JUL-2002
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                                                                                                                                                               119
                                                                                                                                                                                                                                                                222
                                                                                                                                                                                                                                                                                                                                                                                                              AAU96106;
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                                                                                                                                                                                               163
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AAU96106
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P28

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The invention relates to an isolated polynucleotide encoding a variant of the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer membrane protein of E. canis, or an antigenic fragment of the E. canis P30 protein, or comprising a sequence which is the complement of canis and B. chaffeenis and E. chaffeenis outer membrane proteins and their encoding nucleic acids. The polynucleotide 672 of ADA09764. Also disclosed are E. E. chaffeenis outer membrane proteins and their encoding nucleic acids. The polynucleotide protein, for designing hybridiation probes for isolating and identifying CDNA and genomic clones encoding the OMP) or its allelic forms, for designing primers for PCR. The polypeptides encoded by the polynucleotide is useful for diagnosing human ehrlichiosis (Rocky mountain spotted fever) or canine ehrlichiosis. The present
  234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            outer membrane protein, circulating leukocyte, monocytic ehrlichiosis; Rocky Mountian spotted fever; canine ehrlichiosis; antigen.
                                                                                        VNVCYDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNYKRFVVGVTLSTFVFFLSDGAF----SDANFSEGRRGLYIGSQYKVGIPNFSNFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia canis or its variant or fragment, useful for producing Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins diagnosing and treating ehrlichiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide encoding outer membrane protein P30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                YYHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                                                                        sequence represents an E. chaffeensis outer membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.4%; Score 507; DB 6; Length 283; 40.3%; Pred. No. 2.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     chaffeensis outer membrane protein OMP-1B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (OHIS ) UNIV OHIO STATE RES FOUND.
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                                                                                                                                                                                                                                                                                             ADA09737 standard; protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00314701.
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Best Local Similarity 40.3
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlichia chaffeensis.
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                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2003
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                                                              163
                                                                                                                                              222
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                                                                                                                                                                                                                                                                         ADA0973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polynucleotide encoding an outer membrane protein (OMP) of Bhrlichia canis or Bhrlichia chaffeensis used in the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the serum sample and the polypeptide, where formation of a complex is indicative of infection with B. chaffeensis.
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107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            solated polynucleotide encoding an outer membrane protein of E.canis or chaffeensis used in the diagnosis of infection.
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                                                            VNVCYDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLNVNTMLFGGG
                                                                                        BET-IPG---ITKKIFALGLDKSEINTHSNFTRSYDPTYA---SSFAGFSGIIGYYVNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNYKRFVVGVTLSTFVFFLSDGAF-----SDANFSEGRRGLYIGSQYKVGIPNFSNFSA
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Best Local Similarity 40.3%; Pred. No. 2.7e-45;
Matches 116; Conservative 46; Mismatches 100; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   this sequence represents an Ehrlichia outer membrane protein of the
                                                                                                                                                269
                                                                                                                                                                                       281
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane protein; OMP; P30F; ehrlichiosis; infection.
                                                                                                                                                                      YYHGVIGNNFNKIPV-ITPVVLEGAPQTTSALVTIDTGYFGGEVGVRF
                                                                                                                                              YYHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF
                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chaffeensis outer membrane protein (OMP) #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4B; 49pp; English.
                                                                                                                                                                                                                                                                                          ABG77936 standard; protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-2002; 2002US-00059964.
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                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-618954/66.
N-PSDB; ABS63277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKIHISA Y.
OHASHI N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002120115-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                            222
                                                                                                                                                                                     235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OHAS/)
                                                                                                                                                                                                                                                    RESULT 10
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176
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                                               Query Match
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          108 RVEFEGSYENFEPERQWYPENSQS-----YKFFALSRNATNSDNKFIVLENNGVVDKSLN 162
                                         163 VNVCYDIASGSIPLAPYMCAGVGADYIK-FLGISLPKFSYQVKFGVNYPLAVNTMLFGGG 221
                                                                               234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to nucleic acid sequences encoding outer membrane proteins (OMP) of Erlichia chaffeensis (designated as OMP proteins) and Ehrlichia canis (designated as P30F proteins). The OMP polynucleotide is
EET-IPG---ITKKIFALGLDKSEINTHSNFTRSYDPTYA---SSFAGFSGIIGYYNDF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis, useful in preparing a composition for diagnosing or preventing E. canis or E. chaffeensis infection.
                                                                                                                                                                                                                        purification; diagnosis; outer membrane protein; OMP; P30F protein;
                                                                         222 YYHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                                                                                                        Erlichia chaffeensis outer membrane protein (OMP), OMP-1B
                                                                                                                                                                                                                                                                                                                                                          248. .272
/note= "Hypervariable region (HV3)"
                                                                                                                                                                                                                                                                                                                                 /note= "Hypervariable region (HV1)"
                                                                                                                                                                                                                                                                                                        26. .41
/note= "Semivariable region (SV)"
                                                                                                                                                                                                                                                                                                                                        45. .163
note= "Hypervariable region
148. .272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 4; 122pp; English.
                                                                                                                                                                                                                                                                           . .25
'label= Signal_peptide
                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                        ADW04230 standard; protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1998; 98US-0100843P.
19-MAY-1999; 99US-00314701.
28-JAN-2002; 2002US-00059964.
                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-2004; 2004US-00901774
                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                          . 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rikihisa Y, Ohashi N;
                                                                                                                                                                                                                                                 Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-064871/07.
                                                                                                                                                                                                                                  infection; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RIKI/) RIKIHISA Y. (OHAS/) OHASHI N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADW04229.
                                                                                                                                                                                                                                                                                                                                                                                  US2004265334-A1
                                                                                                                                                                                         24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-2004
                                                                                                                                                                         ADW04230;
                                                                                                                                                                                                                                                                   Key
Peptide
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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EET-IPG---ITKKIFALGLDKSEINTHSNFTRSYDPTYA---SSFAGFSGIIGYYVNDF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1. -1(B to Z) shown in AAX06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAX06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs. (Updated
                                                                                                                                                                                                                                                                                                     9
useful in preparing a composition for diagnosing, treating or preventing an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present sequence is the Erlichia chaffeensis OMP protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia
                                                                                                                                                                                                                                                                                        RVEFEGSYENFEPERQWYPENSQS - - - - YKFFALSRNATNSDNKFIVLENNGVVDKSLN
                                                                                                                                                                                                                                                      1 MNYKRFVVGVTLSTFVFFLSDGAF-----SDANFSEGRRGLYIGSQYKVGIPNFSNFSA
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRP 269
                                                                                                                                                     Length 283;
                                                                                                                                                  35.4%; Score 507; DB 9; Length 28: 40.3%; Pred. No. 2.7e-45; ive 46; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 17B; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US019600.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. chafeensis OMP-1Y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                  Best Local Similarity 40.3
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-254290/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX34757
                                                                                                        Sequence 283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9913720-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-2003
05-JUL-1999
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10;

Gaps

26;

118 160 175

109

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The invention relates to an isolated polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used in the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the serum sample and the polypeptide, where formation of a complex is indicative of infection with E. chaffeensis. This sequence represents an Ehrlichia outer membrane protein of the
                                                                                                                                                                                                   161 LNVNVCYDIASGSIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGG 220
                                                                                                                                                                                                                   Isolated polynucleotide encoding an outer membrane protein of E.canis or E.chaffeensis used in the diagnosis of infection.
                                                                                   57 T-----IPGITKKIFALGLDKSBINTHSNFTRSYDPTYASSFAGFSGIIGY-YVNDFRV
                                                       1 MNNRKSFFIIGASLLASLLFTSBASSTGNVSNHTYFKPRLYISGOYRPGVSHFSKFSVKE
                                                                                                                                             110 EFEGSYENFEPERQWYPENS--QSYKFFALSR-----NATNSDN--KFIVLENNGVVDKS
                                                                                                                                                            119 EVEASYEEFDVKN---PEGSATDAYRYFALARAMDGTNKSSPDDTRKFTVMRNDGLSISS
                             MNYKR--FVVGVTLSTFVFFLSDGAFSD--ANFSEGRRGLYIGSQYKVGIPNFSNFSAEE
                                                                                                                 61 TNYNTTQLVGLKKDISVIG--NSNITTYTNFNFPYIAEFQDNAISFSGAIGYLYSENFRI
                                                                                                                                                                                                                                                           GYYHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                                                                                                                                                                             Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Outer membrane protein; OMP; P30F; ehrlichiosis; infection
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia chaffeensis outer membrane protein (OMP) #15
 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 494; DB 5;
Pred. No. 6.8e-44;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                               Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Fig 17B; 49pp; English
                                                                                                                                                                                                                                                                                                                                                              ABG77949 standard; protein; 285
 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2002; 2002US-00059964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00314701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.4%;
38.4%;
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rikihisa Y, Ohashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-618954/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKI/) RIKIHISA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OHAS/) OHASHI N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABS63290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002120115-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2002.
 111;
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                                                                                                                                                                                                                                                           221
                                                                                                                                                                                                                                                                                      236
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  Matches
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ABG77949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins (P28-1 to P28-21) of Ehrlichiā chaffeensis. P28 proteins are encoded by a 28kDa outer membrane protein multigene family. P28 proteins are useful as a vaccine against E.Chaffeensis. DNA encoding P28 is useful for transfecting a host cell. AAU73420 represent Ehrlichia chaffeensis P28 outer membrane proteins of the invention
                                                                                                                 26
                                                                                                                                             9
                                                                                                                              THYNTTQLVGLKKDISVIG--NSNITTYTNFNFPYIAEFQDNAISFSGAIGYLYSENFRI
                                                                                                                                                                                                                                                 LNVNVCYDIASGSIPLAPYMCAGVGADYIKFLGISLPKFSYQVKFGVNYPLNVNTMLFGG
                                                                                                                                                                                                                                                                                                                 VMINGCYNFTLDDIPVVPYVCAGIGGDFIEFFNDLHVKFAHQGKVGISYSISPEVSLFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia chaffeensis 28-kDa outer membrane protein, designated
l as a vaccine against Ehrlichia chaffeensis.
                                                                                                                 MNYKR--FVVGVTLSTFVFFLSDGAFSD--ANFSEGRRGLYIGSQYKVGIPNFSNFSAEE
                                                                                                                                                                      T-----IPGITKKIFALGLDKSEINTHSNFTRSYDPTYASSFAGFSGIIGY-YVNDFRV
                                                                                                                                                                                                                                EFEGSYENFEPERQWYPENS--QSYKFFALSR-----NATNSDN--KFIVLENNGVVDKS
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to isolated and purified 28-kDa outer membrane
                                                                                    26;
                                                                                                                                                                                                                                                                                                                                               GYYHKVVGDRHERVEIAYHPTALSDVPRTTSASATLNTDYFGWEIGFRF 269
                                                                                                                                                                                                                                                                                                                                                               Ehrlichia; outer membrane protein; P28; antibiotic; vaccine.
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                                                        Length 285;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia chaffeensis outer membrane protein P28-9
                                                                                   95;
                                                       Query Match

34.4%; Score 494; DB 2;
Best Local Similarity 38.4%; Pred. No. 6.8e-44;
Matches 111; Conservative 57; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 494; DB 5;
Pred. No. 6.8e-44;
 correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEV FOUND
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Best Local Similarity
 on 27-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu X;
                            Sequence 285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 285 AA
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26; Gaps

95; Indels

57; Mismatches

Matches 111; Conservative

Search completed: December 28, 2005, 15:36:01 Job time: 92 secs

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December 28, 2005, 10:46:11; Search time 197 Seconds (without alignments) 7335.826 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6E_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6E_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/6E_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/RTUSCOMB.seq:*

7: /cgn2_6/ptodata/1/ina/RECOMB.seq:*

8: /cgn2_6/ptodata/1/ina/RECOMB.seq:*

9: /cgn2_6/ptodata/1/ina/RECOMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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813
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 25, Sequence 25, Sequence 41, Sequence 41, Sequence 47, Sequence 23, Sequence 23, Sequence 23, Sequence 25, Sequence 45, Sequence 45, Sequence 47 Sequence 47 Description Sequence 6 Sequence 6 Sequence 6 Sequence 4 Sequence 2 Sequence 2 Sequence 2 Sequence Seq US-09-660-587-45
US-09-811-007A-45
US-09-314-701-23
US-10-314-701-23
US-10-059-964A-23
US-10-059-964A-25
US-10-059-964A-25
US-10-059-964A-47
US-09-314-701-47
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US-10-059-964A-61
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US-10-059-964A-27
US-09-314-701-59
US-10-059-964A-27
US-09-314-701-59
US-10-059-964A-27 SUMMARIES B Query Match Length Score 162.2 162.2 150.2 150.8 150.8 150.8 147.2 147.2 146.6 146.6 146.6 Result No. 

Sequence 5, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli	3, A
US-10-314-639-5 US-10-059-964A-5 US-08-953-326-9 US-09-314-701-9 US-10-314-639-9 US-10-062-994-9 US-10-01-31 US-10-314-639-9 US-10-059-964A-31 US-10-314-639-31 US-10-059-964A-31 US-09-314-701-11 US-09-314-701-11 US-09-553-662-10 US-10-059-964A-11 US-09-314-701-11 US-09-314-10-11 US-10-314-639-11	US-10-059-964A-51 US-09-314-701-3
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RESULT 3
US-09-314-701-23
i Sequence 23. Application US/09314701
i Patent No. 6544517
i GENERAL INFORMATION:
i APPLICANT: Rikihisa, Yasuko
i APPLICANT: Rikihisa, Yasuko
i TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
i TITLE OF INVENTION: Chaffeensis
i FILE REFERENCE: 2727/04021
i CURRENT APPLICATION NUMBER: US/09/314,701
i CURRENT FILING DATE: 1999-05-19
i NUMBER OF SEQ ID NOS: 66
i SOFTWARE: PatentIn Ver. 2.0
i SEQ ID NO 23
i LENGTH: 840
                                                                               ATTACAAAAAAGATTTTTGCGTTAGGTCTTGATAAGTCTGAGATAAATACTCACAGCAAT 240
                                                                                                                                             TITACACGATCATATGACCCTACTTATGCAAGCAGTTTTGCAGGGTTTAGTGGTATCATT 300
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                  CAGTATAAAGTTGGTATTCCCAATTTTAGTAATTTTTTCAGCTGAAGAAACAATTCCTGGT
                                                              ATTACAAAAAAGATTTTTGCGTTAGGTCTTGATAAGTCTGAGATAAATACTCACAGCAAT
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 CAGTATAAAGTTGGTATTCCCAATTTTTAGTAATTTTTCAGCTGAAGAAACAATTCCTGGT
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ORGANISM: Ehrlichia chaffeensis
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APPLICANT: Walker, David H.

APPLICANT: Walker, Jere W.

APPLICANT: W. Xue-Jie

JAPLICANT: W. Xue-Jie

TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein

TITLE OF INVENTION: Genes of Bhrlichia canis and Uses Thereof

TITLE OF INVENTION: US/09/811,007A

CURRENT APPLICATION NUMBER: 09/660,587

PRIOR FILING DATE: 2000-09-12

PRIOR FILING DATE: 2000-09-12

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 45

LENGTH: 813
                                                                                                                                                                                           CTTAATGTAAATGTTTGTTATGATATTGCTAGTGGTAGTATTCCTTTAGCACCTTATATG
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US-09-811-007A-45
Sequence 45, Application US/09811007A
Patent No. 6660269
GENERAL INFORMATION:
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APPLICATION NUMBER: US/09/314,701
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Patent No. 6893640

GENERAL INFORMATION:
APPLICANT: Rikhisa, Yasuko
APPLICANT: Chast, No. 689364010

TITLE OF INVENTION: Chaffeensis
FILE REFERENCE: 22727/04012

FILE REFERENCE: 22727/04012

CURRENT APPLICATION NUMBER: US/10/314,639

CURRENT APPLICATION NUMBER: US/10/314,639
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 Score 162.2; DB 3; Length
Pred. No. 9.4e-32;
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                                                                                                                                                                                  TYPE: DNA
ORGANISM: Ehrlichia chaffeensis
PRIOR APPLICATION NUMBER: US/09,
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 840
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Best Local Similarity 53.8%;
Matches 432; Conservative
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US-10-314-639-23
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TGGTGCAGATTATATAAAGTTTTTAGGTATATCATTGCCTAAGTTTTCTTATCAAGTTAA 611
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                                                                                               APPLICANT: ORASHI, NORION
TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA
TITLE OF INVENTION: CHAFFENSIS
FILE REFERENCE: 22727-04109
CURRENT APPLICATION NUMBER: US/10/059,964A
CURRENT FILING DATE: 1090-01-28
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PALENTIN VET. 3.2
LENGTH: 840
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Pred. No. 9.4e-32;
0; Mismatches 353;
                                        Sequence 23, Application US/10059964A Patent No. 6923963 GENERAL INFORMATION:
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53.8%;
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Matches 432; Conservative
                                                                                        APPLICANT: RIKIHISA,
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                                                                                                                                                                                                                                                                                                              TYPE: DNA
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Pred. No. 7.5e-29;
0; Mismatches 307;
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Patent No. 6544517
GENERAL INFORMATION:
APPLICANT: Rikihisa, Yasuko
ITILE OF INVENTION: Outer Membrane Protein of
ITILE OF INVENTION: Chaffeensis
FILE REFERENCE: 22727/04021
CURRENT APPLICATION NUMBER: US/09/314,701
CURRENT PILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 852
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APPLICANT: OHASHI, NORIO
TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA
TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA
FILE REFERENCE: 22727-04109
CURRENT APPLICATION NUMBER: US/10/059,964A
CURRENT FILING DATE: 09/314,701
PRIOR FILING DATE: 1998-05-19
PRIOR PILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PATENTIN Ver. 3.2
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 25
LENGTH: 052
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                            471 AACAAATAAGTATGTTGTTATAAAGAACAATGGCTTATCTGTCGCATCCATTATAATCAA
                                                              Length 852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 25, Application US/10059964A; Patent No. 6923963; GENERAL INFORMATION:
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ORGANISM: Ehrlichia chaffeensis
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US-10-059-964A-25
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Best Local S
Matches 402
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Sequence 25, Application US/10314639
Patent No. 6893640
GENERAL INFORMATION:
APPLICANT: RIKIAIDS AND ASSET APPLICANT: Obasi, No. 6893640io
TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia TITLE OF INVENTION: Chaffeensis
TITLE OF INVENTION: Chaffeensis
TITLE OF INVENTION: Chaffeensis
CURRENT APPLICATION NUMBER: US/10/314,639
CURRENT FILING DATE: 2002-12-09
PRIOR PILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
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TAAGGTTGTAGGTGATAGGCATGAGAGTAGAAATAGCTTACCATCCTACTGCATTATC 731
                                                                                                                                                    TAAGGTCATAGGAAATAAATTTAACAATTTAAATGTTCAACACGTTGTTAGTCTTAACAG 770
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                                                   GTTTGGTGTCAACTACCCTCTAAATGTTAATACTATGTTGTTTGGTGGGGGTTATTACCA
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ORGANISM: Ehrlichia chaffeensis
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828 ATTTGGGTTAAAATTT 843
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Best Local Similarity 54.64
Matches 402; Conservative
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; LOCATION: (1)..(852)
US-10-314-639-25
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US-10-314-639-25
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Sequence 41, Application US/09811007A

Patent No. 6660269

GENERAL INFORMATION:

APPLICANT: Walker, David H.

APPLICANT: Walker, Jere W.

APPLICANT: Yu, Xue-Jie

TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein

TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof

TITLE OF INVENTION: 2001-10-23

CURRENT APPLICATION NUMBER: US/09/811,007A

CURRENT APPLICATION NUMBER: 09/660,587

PRIOR APPLICATION NUMBER: 09/660,587

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 41

LENGTH: 840
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                             121 ATTAGTGCAAAGTACAATCCAAGTATATCACACTTTAGAAAATTCTCTGCTGAAGAAACT
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                                                                                                          cctattaatggaacaaattctctcactaaaaaagttttcggactaaagaaaatggtgat
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                                                                            ATTCCTGGTATTACAAAAAGATTTTTGCGTTAGGTCTTG----
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 AGAATTTGAAGGTTCTTATGAGAATTTTGAACCTGAAAGACAATGGTACCCTGAGAATAG 386
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APPLICANT: Walker, David H.
APPLICANT: Walker, Jere W.
APPLICANT: Wolve-Jie W.
APPLICANT: Yu, Xue-Jie W.
APPLICANT: Yu, Xue-Jie W.
APPLICANT: Yu, Xue-Jie W.
APPLICANT: Title OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE RFERENCE: D6152CIP2
CURRENT APPLICATION NUMBER: US/09/660,587
PRIOR APPLICATION NUMBER: 09/261,358
PRIOR APPLICATION NUMBER: 09/261,358
NUMBER OF SEQ ID NOS: 46
                                                                          387 CCAAAGCTACAAATTTTTTGCTTTGTCTCGAAATGCTACAAATAGTGAT----
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Best Local Similarity 53.2%; Pred. No. 6.2e-28;
Matches 445; Conservative 0; Mismatches 358;
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Patent No. 6392023
GENERAL INFORMATION:
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LENGTH: 840
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Batent No. 6544517

BAPLICANT: Rikihisa, Yasuko
APPLICANT: Rikihisa, Yasuko
APPLICANT: Obsai, No. 6544517io
TITLE OP INVENTION: Chaffeensia
FILLE REFERENCE: 22727/04021
CURRENT APPLICATION WUBBE: US/09/314,701
CURRENT FILLNG DATE: 1999-05-19
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Score 147.2; DB 3;
Pred. No. 6.2e-28;
0; Mismatches 358;
 Query Match
Best Local Similarity 53.2%;
Matches 445; Conservative
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Pred. No. 6.2e-28;
0; Mismatches 358;
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ilarity 53.2%;
Conservative
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                           TYPE: DNA
ORGANISM: Ehrlichia
                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)..(843)
US-09-314-701-47
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SEQ ID NO 47
LENGTH: 843
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us-10-731-554-45.rn1

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Query Match
18.1%;
Best Local Similarity 53.2%;
Matches 445; Conservative (
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APPLICANT: Ohsel, No. 689364010

TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia and Ehrlichia
TITLE OF INVENTION: Chaffeensis
FILE OF INVENTION: Chaffeensis
FILE OF INVENTION: Chaffeensis
CURRENT APPLICATION NUMBER: US/10/314,639
CURRENT FILING DATE: 2002-12-09
PRIOR PILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 47
LENGTH. 843
TYPE: ....
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                                                                                                                                                                                                                                                                                                                                                               Length 843;
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                                                                                                                                                                                                                                                                                                                                                              Score 147.2; DB 3;
Pred. No. 6.2e-28;
0; Mismatches 358;
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                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 53.2
Matches 445; Conservative
                                                                                                                                                                                                                                                                         ORGANISM: Ehrlichia canis
                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)..(843)
US-10-314-639-47
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Sequence 47, Application US/10059964A
Patent No. 622363
GENERAL INFORMATION:
APPLICANT: RIKHLSA, YASUKO
APPLICANT: RIKHLSA, YASUKO
APPLICANT: OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA
TITLE OF INVENTION: CHAFFERNSE;
FILE REFERRACE: 22727-04109
CURRENT APPLICATION NUMBER: US/10/059,964A
CURRENT FILING DATE: 1999-05-119
PRIOR PLILOR DATE: 1999-05-119
PRIOR PLILOR DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAGGTAGTCAGTATAAAGTTGGTATTCCCAATTTTAGTAATTTTTCAGCTGAAGAACA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATTAGTGCAAAGTACAATCCAAGTATATCACACTTTAGAAAATTCTCTGCTGAAGAACT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAMATACTCACAGCAATTTTACACGATCATATGACCCTACTTAT-----GCAAGCAGT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAACAAAAAAAGACGATTTTTACAAGAGTAGCTCCAGGCATTGATTTTCAAAATAACTTA 300
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                                                                              CATGAGAGAGTAGAAATAGCTTACCATCCTACTGCATTATCTGACGTTCCTAGAACTACT
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Pred. No. 6.2e-28;
0; Mismatches 358;
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Sequence 61, Application US/10314639
Fatent No. 6893640
GENERAL INFORMATION:
GENERAL INFORMATION:
TYPICANT: RIKINISA Yasuko
TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
TITLE OF INVENTION: Chaffeensis
TITLE OF INVENTION: Chaffeensis
TITLE OF INVENTION: Chaffeensis
TITLE OF INVENTION WHERE: US/10/314,639
CURRENT FILING DATE: 2002-12-09
FILE REPERIOR APPLICATION NUMBER: US/09/314,701
PRIOR APPLICATION NUMBER: US/09/314,701
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOOTHWARE: PATENTIN Ver. 2.0
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                                                                                                             565 ATAAAGITITITAGGTATATCATTGCCTAAGITTTCTTATCAAGTTAAGITTGGTGTCAAC 624
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GAGGCATTGTTTGGGCTAAAACAAGATATTAGTTCTATTTTACGTAATAAAGAGACCACA
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                                                                                                                                        ATTGCTAGTGGTAGTATTCCTTTAGCACCTTATATGTGTGCTGCTGGTGTGCTGCTGATTAT
                                                                           415 ATTICITIAAAIGATICIAAGGIGICACCITACATATGCACAGGGTITGGIGGAGATTIT
                                                                                                                                                                                               TACCCTCTAAATGTTAATACTATGTTGGTGGGGGGTTATTACCATAAGGTTGTAGGT
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Pred. No. 8.4e-28;
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Best Local Similarity 54.0%;
Matches 358; Conservative
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; LOCATION: (1)..(726)
US-10-314-639-61
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ORGANISM: p30-12
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                                                                                                 541 GCTGAAGGAGTATCTTTCGTACCATGTGCAGGTATAGGAGCAGATCTTATCACT 600
                                                                                                                                                                                                                     631 CTANATGTTAATACTATGTTGTTGGTGGGGGTTATTACCATAAGGTTGTAGGTGATAGG 690
                                                                                                                                                                                                                                                       Arcaccacagaagrcrcrccarrrarrggrcgaracraccargccgrrarrggraaraa 720
                                                                                                                                                                                                                                                                                                691 CATGAGAGAGTAGAAATAGCTTACCATCCTACTGCATTATCTGACGTTCCTAGAACTACT 750
                                                                                                                                                                                                                                                                                                                                     TTTGAGAAGATACCTGTA---ATAACTCCTGTAGTATTAAATGATGCTCCTCAAACCACA 777
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  CTTAAAAATGACGCATAACTTTTATGTCATTGATGGTTAATACTTGCTATGCATTACA
                                                               511 AGTGGTAGTATTCCTTTAGCACCTTATATGTGTGCTGGTGTTGGTGCTGAATTATATAAAG
                                                                                                                                          TCAGCTICTGCTACTTTAAATACTGATTATTTTGGTTGGGAGATTGGATTTAGATT 806
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Patent No. 6544517
GENERAL INFORMATION:
APPLICANT: Richiesa Yasuko
TITLE OF INVENTION: Outer Membrane Protein of
TITLE OF INVENTION: Chaffeenis
FILE REPRENCE: 22727/04021
CURRENT APPLICATION NUMBER: US/09/314,701
CURRENT FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
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Matches 358; Conservative
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US-09-314-701-61
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Unclassified.
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1 (bases 1 to 13)
Walker, D.H., Yu, X.-J. and McBride, J.W.
Homologous 28-kilodalton immunodominant prccanis and uses thereof
Patent: US 6660269-A 45 09-DEC-2003;
Research Development Foundation; Carson Cit
Location/Qualifiers
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Sequence 45 from patent US 6660269.
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AF078553 Ehrlichia
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                      GenCore version 5.1.6
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DNA

protein genes of Ehrlichia

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TITLE Direct Submission JOURNAL Submitted (04-AUG-2000) Pathology, University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA REMARK Sequence update by submitter COMMENT On Sep 18, 2000 this sequence version replaced gi:3769522. FEATURES Location/Qualifiers Source //organism="Ehrlichia canis" //mol_type="genomic DNA" // Brain="Jake" // Ab_xref="taxon:944"	/gene="p28a" <1146 /gene="p28a" /note="outer membrane protein" /codon_start=3 /transl_table=11 /product="p28" /protein id="AAG14355.1" /db_xref="G1:10181083"	/translation="SIISHYSVKNLFVQYVNTLEEYPRVTSAIATLDIGYLGGEIGIR PIF: 1701051 /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1" /gene="p28-1"	/protein_i="Add14356.1" //protein_i="Add14356.1" //protein_i="ManNELKET" //db_xref="G1:10181084" //db_xref="G1:10181084" //refaulation="ManNELKET" //refaulation="ManNELKET" //refaulation="ManNELKET" //refaulation="ManNELKET" //refaulation="ManNELKET" //refaulation="ManNELKET" //refaulation="ManNELKET" //refaulation="ManNELKET" //refaulation="ManNELT" //refaulation	ψ.	CDS 27693599  /gene="po8="po8=") /note="po8="yes=") /codon_start=1 /cranal_table=11 /product="po8=3" /protein_id="Aad14358.1" /db_xref="d1:10181086" /db_xref="d1:10181086" /translation="MNCKKILITTTLVSLTILLPGISFSKPIHENNTTGNFYIIGKYV PSISHFGNFSAKEEKNTTTGIFGLKESATGGILDKEHAAFNIPNYSFKYENNPFLGF AGVIGYSIGSPRIEFEVSYETPDVQNPGDKFNNDAHKYCALSNDSSKTMKSGKFVFLK NEGLSDISLMLAVCYDLINKRNPFSPYICAGIGTDLIPMFDAINHKAAYOGKLGFNYP ISPEANISMGVHFHKVTNNBFRVPVLLTAGGLAPDNLFAIVKLSICHFGLEFGYRVSF "GPEANISMGVHFHKVTNNBFRVPVLLTAGGLAPDNLFAIVKLSICHFGLEFGYRVSF	gene 38104673 /gene="p28-4"
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10127

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10187

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gene

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GLYKPS VSHRSDFS IKETYTNTEALFGLKQDISS ILRNKETTOYNNFNVPYTAKFOD
BASS PSE AN UCYL IANNOFN IEL BGS YEBED VKNPGNYTT I DAHRY I ALLAREKTS YYLSS
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                                                                                                                                                                                                Yu,X.J., McBride,J.W., Zhang,X. and Walker,D.H.
Characterization of the complete transcriptionally active Ehrlichia
chaffeensis 28 kDa outer membrane protein multigene family
Gene 248 (1-2), 29-68 (2000)
3 (bases 1 to 1268)
Yu,X.J., McBride,J.W. and Walker,D.H.
                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                   of Texas Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGYYHKVIGRRYERVEIAYHPATLTNVPKTTSASATLDTDYFGWEVGMRFTL"
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1 (bases 1 to 2977)
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Submitted (26-MAY-1998) Pathology, The University of Texas
Branch, 301 Univ. 1998) Pathology, The University of Texas
4 (Dases 1 to 2977)
Yu,X.J., McBride,J.W., Zhang,X. and Walker,D.H.
Direct Submission
Submitted (01-FBB-2000) Pathology, University of Texas Med
Branch, 301 Univ. Blvd., Galveston, TX 77555, USA
Sequence update by submitter
On May 24, 2000 this sequence version replaced gi:3192922.
Location/Qualifiers
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                                                                          Yu, X.J., McBride, J.W. and Walker, D.H.
Genetic diversity of the 28-kilodalton outer
in human isolates of Ehrlichia chaffeensis
J. Clin. Microbiol. 37 (4), 1137-1143 (1999)
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On or before Apr 2, 2001 this sequence version replaced gi:2853584,
gi:2853273.
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Ohashi,N., Zhi,N., Zhang,Y. and Rikihisa,Y.
Direct Submission
Submits (1997) Department of Veterinary Biosciences, The Ohio State University, 1925 Coffey Rd., Columbus, OH 43210-1093,
                                                                                                                                                                                                                                                                                                                                                                                             of Veterinary Biosciences, The Rd., Columbus, OH 43210-1093,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohashi, N., Rikihisa, Y. and Unver, A.
Direct Submission
Submitted (29-NOV-2000) Department of Veterinary Biosciences, Th
Ohio State University, 1925 Coffey Rd., Columbus, OH 43210-1093,
                                                                                                                                                                                                          Ω.
Ohashi,N., Zhi,N., Zhang,Y. and Rikihisa,Y.
Immunodominant major outer membrane proteins of Ehrlichia
Chaffeensis are encoded by a polymorphic multigene family
112-139 (1998)
                                                                                                                                                            2 (bases 1 to 27190)
Mosshi, V., Rikihisa, Y. and Unver, A.
Analysis of transcriptionally active gene clusters of maj
membrane protein multigene family in Ehrlichia canis and '
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Ohashi,N., Zhi,N., Zhang,Y. and Rikihisa,Y.
Direct Submission
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Ohio State University, 1925 Coffey
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/strain="Arkansas"
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Anaplasmatecese; Ehrlichia.
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Pred. No. 6.5
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SQTIQYFSKALALLEABGCYQEFNVYNSNNSLIJSNKYHSHTBNPATTYNTSIS
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                                           23091 GAAAGACAGTGGTATCCTGAAGGAGAGAAGCCATAAGTTTTTTGCTCTATCTCGTGAG 23032
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                                                                                                                                                                                   23031 TCCACTGTTCAAGATAATAAGTTTATAGTGTTAGAAAATGATGGTGTTATTGATAAATCT
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                                                                                                             GCTACAAATAGTGATAATAAGTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCT
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1 (bases 1 to 21115)
Martinez, D., Ferraz, C., Demaille, J., Bensaid, A. and Frutos, R. Analysis of the major antigenic protein 1 multigene family of Ehrlichia ruminantium strain Gardel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia ruminantium
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
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Martinez,D., Ferraz,C., Demaille,J., Bensaid,A. and Frutos,R.
Direct Submission
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Ehrlichia ruminantium strain Gardel Mapl cluster, complete
Ehrlichia ruminantium (heartwater rickettsia)
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                                                                                                                                            12401. .13273
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                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 229;
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Pred. No. 8.8
                                                                                                                                                                                        /codon_start=1
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Best Local S
Matches 578
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TCTGCTACTTTAAATACTGATTATTTTGGTTGGGAGATTGGATTTAGATTT 807

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Characterization of a major outer membrane protein multigene family in Ehrikotha ruminantium
an Ehrikotha ruminantium
Gene 330, 159-168 (2004)
2 (bases 1 to 24993)
van Heerden, H., Collins, N.E. and Allsopp, B.A.
Direct Submission
Submitted (16-JUL-2003) Onderstepoort Veterinary Institute,
Molecular Biology Section, 100 old Soutpan Road, Onderstepoort
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAR10930.1"
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                                                                                                                                                                                                                                    Ehrlichia ruminantium hypothetical transcriptional regulator gene, complete cds; mapl locus, complete sequence; secA gene, partial AY33131
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idskevlmmyraytciknekvrniiynlykalstdnktsvs"
                                                                        756
                           56982 AGGGTAAAAGTGGTTTATCATCCTGTTCAGTTAAATACTGTTCCTAAAATGACATTTGTT
           GTTAATACTATGTTGTTGGTGGGGGTTATTACCATAAGGTTGTAGGTGATAGGCATGAG
                                                                        CCTAGAACTACTTCAGCT
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
1 (bases 1 to 24993)
van Heerden,H., Collins,N.E., Brayton,K.A., Rademeyer,C. and
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                                                                                                                                     757 TCTGCTACTTTAAATACTGATTATTTTGGTTGGGAGATTGGATTTAGATTT 807
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Bhrlichia ruminantium
                                                                          AGAGTAGAAATAGCTTACCATCCTACTGCATTATCTGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 24993
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/strain="Welgevonden"
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AUTHORS
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JOURNAL
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CR925677 Accession CR925677
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Pred. No. 5.1e-61;
0; Mismatches 229;
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510000
610000
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Matches 578; Conserv
                                                                                                            Sequence split into
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CR925677 00
CR925677 01
CR925677 03
CR925677 03
CR925677 04
CR925677 06
CR925677 06
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ISYRESPKISLFIDGYYHHIIGNQPKNLSVHHAVELSEFPKNSSAVATLDIGYLGGEV
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product="MAP1-2"
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Best Local Similarity
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LPNLALFVDGSFYSHLSNKFTHI PTIN IMDPPILPDSSSAKFNVNFLSSSFGIRFIH"
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                                                                                                                                    GGTATTACAAAAAAGATTTTTGCGTTAGGTCTTGA-----TAAGTCTGAGATAAATACT
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                                                                                                                                                           Length 110000
                                                                                                                                                                                                30;
                                                                                                                                                                                                Indela
                                                                                                                                                           Score 380.6; DB 1;
Pred. No. 6.1e-60;
0; Mismatches 229;
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	AF319940 19449 bp DNA linear BCT 05-JUL-2005 Ehrlichia ruminantium isolate Senegal mapl gene cluster, partial Bequence. AF319940 AF319940.4 GI:66957871	Ehrlichia ruminantium (heartwater rickettsia) Ehrlichia ruminantium Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia. 1 (bases 1 to 19449) Bekker, C.P., Bell-Sakyi, L., Paxton, E.A., Martinez, D., Bensaid, A.	Transcriptional analysis of the major antigenic protein 1 multigene family of Cowdria ruminantium Gene 285 (1-2), 193-201 (2002) 12039046 2 (bases 1 to 19449)	Bekker, C.P., Postigo, M., Taoufik, A., Bell-Sakyi, L., Ferraz, C., Martinaz, D. and Jongejan, F. Transcription Analysis of the Major Antigenic Protein 1 Multigene Family of Three In Vitro-Cultured Bhrlichia ruminantium Isolates J. Batteriol. 187 (14), 4782-4791 (2005)	John State Lo 19449)  Sheker, C.P. J., Paxton, E.A., Bell-Sakyi, L., Martinez, D., Bensaid, A. and Jongejan, F.  Briter, Submission Submitted (OT-NOV-2000) Bacteriology, Faculty of Veterinary	4 (bases 1 to 1944) Bekker, C.P.J., Taoufik, A. and Jongejan, F. Direct Submission Submitted (09-NOV-2004) Virology, Utrecht University, Yalelaan 1,	Utrecht 3584CL, The Netherlands Sequence update by submitter On Jun 6, 2005 this sequence version replaced gi:55620638. Location/Qualifiers		/gene="map1-14" /gene="map1-14" /note="member of multigene family" /codon start=1 /cransl_table=11 /product="MAP1-14" /protein_id="AAY59045.1" /db xref=[3[166957874"	YTSGQYSIELDIA GANANYA YTSGQYSIELDIA GANANYAHENGDKELTIESLKERNELKIANDKGGFKKGYNEVYN RNYTGFSGALGYSGCGLRIELGGAFTKFDUNKQYKKFODNRPYFALSKOBEISGOPDO PTPTPPPPPPPPPPPPPPTTTTIELGGAFTKFODNRPYFALSKOBEISGOPDO PTPTPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP
07 do 20	RESULT 12 AF319940/C LOCUS DEFINITION ACCESSION	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL PUBMED REFERENCE	AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	REMARK COMMENT FEATURES SOUTCE	gene	3	gene
into 16 fragment e Begin 100001 200001 300001 400001	CR925678_05 500001 610000 CR925678_06 600001 710000 CR925678_09 800001 910000 CR925678_09 900001 910000 CR925678_09 900001 1010000 CR925678_10 1000001 1110000 CR925678_11 1100001 1210000 CR925678_11 1100001 1310000	1300001 1410000 1400001 1510000 1500001 1512977 of 16) of CR925678 from base 1400001 (CR925678 Ehrlichia rum 46.8%; Score 380.6; DB 1; Length 110000; larity 69.1%; Pred. No. 6.1e-60;	1 ATGAATTACAAAAGATTTGTTGTAGGTGTTACGCTGAGTACATTTGTTTT  1 ATGAATTATAAAGAATTTGTTGTAGGTGTTACGCTGAGTACATTTGTTTT  11320 ATGAATTATAAGGAATTTGTTTTAGGTGTTACATTAAGTGCATTGTTGTT	Qy         59 -CTGATGGTGCTTTTTCTGAAGGGAGGAGGAGCTTTATATAGGT 117	Db 71200 GTTCAGTATAGAAAATTTTGATAATTTTTTTTTTTCAGAAAAAAATTTT1  Qy 178 GGTATTACAAAAAGATTTTTGCGTTAGGTCTTGATAGGTCTGAGAAAATATT 231	232 CACAGCAATTTTACACGATCATATGACCCTACTTATGCAAGCAGTTTTGCAGGGTTTAGT	OY 292 GGIRICATIGGATATTAIGTTAAGGGRAGAATTTGAAGGTTCTTATGAGAAT 351		Oy         451         CTAGAGAATAACGGCGTTGTTGACAAGTCTCTTAATGTAAATGTTATGTTATGTTATGTT 510           Db         70840         TTGGAAATAATGGGGTTAAGAACTTAGCACTTGCATGTAATTTTTGTTGTTGTT         70781           Oy         511         AGTGGTAGTATTCCTTTAGCACCTTAATATGTGTGCTGGTGGTGGGGAATTATATAAAG         570           Db         70780         CACGGAAAATATTCCTTTAGGACCTTAACGTGTGTGCTGGTTGGT	QY 571 TTTTAGGTATATCATTGCCTAAGTTTTCTTATCAGTTAGGTGTCAACTACCCT 630

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19427 ingrinicrinachachachacharanananan 19368
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AYQAKLGISYYISPSVNLFADIYYHKSVGNQFKNLRVQYAHTLRLTPIFTSAIAKLNI
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VMKNTGLSMTSVMFNGCYNILSNKLEISPYVCIGIGGDFIDFPDATHIKLAYQGKLGI
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RS Rikhisay. and Ohashi, N.

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            Outer membrane protein of Ehrlichia canis and Ehrlichia (Patent: US 6893640-A 23 17-MAY-2005;
The Ohio State University Research Foundation; Columbus,
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Pred. No. 1.3e-19;
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RESULT 15 ECU72291

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EFNDKKGYSPIYNRNYTGFSGAIGYSGGGLRVELEGAFTRFDVDKQKYKKDNYRYFAL
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On or before Apr 2, 2001 this sequence version replaced gi:2853584,
gi:2853273.
                                 BCT 02-APR-2001 membrane protein
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Ohashi,N., Rikhisa,Y. and Unver,A.
Direct Submission
Submitted (29-NOV-2000) Department of Veterinary Biosciences, Th
Ohio State University, 1925 Coffey Rd., Columbus, OH 43210-1093,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (27-AUG-1997) Department of Veterinary Biosciences, Th
Ohio State University, 1925 Coffey Rd., Columbus, OH 43210-1093,
                                                                                                                                                                                                                                                                                                                            Rickettsiales
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Ohashi,N., Rikihisa,Y. and Unver,A.
Analysis of transcriptionally active gene clusters of major membrane protein multigene family in Ehrlichia canis and E.
chaffeensis
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ene family
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1 (bases 14844 to 21136; 21479 to 22234)

Chashi,N., Zhi,N., Zhang,Y. and Rikhinsa,Y.

Immunodominant major outer membrane proteins of Ehr

Chaffensis are encoded by a polymorphic multigene:

Infect. Immun. 66 (1), 132-139 (1998)
Ebrlichia chaffeensis strain Arkansas major outer omp-1 multigene cluster, complete sequence.

172291 AF021338
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Ohashi,N., Zhi,N., Zhang,Y. and Rikihisa,Y.
Direct Submission
Submitted (24-SEP-1996) Department of Veter:
Ohio State University, 1925 Coffey Rd., Colv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (bases 1 to 27190)
Ohashi,N., Zhi,N., Zhang,Y. and Rikihisa,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
  SIMVNTCYDISINNTSIVPYLCTGIGEDLVGLFNTIHFKLAYQGKVGMSYLINNNILL
FSDIYYHKVMGNRFKNLYMQYVADPNISEETIPILAKLDIGYFGSEIGIRFMFN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7591 CATTTTAGCAATTTCTCAGTAAAGAAACTAATGTTGATACAATACAACTAGTAGGATAT 7650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTACTTGCATCTCTATTATCATTCTTATCTATTGAATCCTTTTCAGCTATAAATCATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AATTTTAGTAATTTTTCAGCTGAAGAAACAATTCCTGGTATTACAAAAAAAGATTTTTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 AATTITICIGAAGGAGGAGAAGACTITAATATAGGTAGTCAGTATAAAGTIGGTATTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7531 CATACAGGAAATAACACTAGTGGTATATATTACAGGGCAGTATAGACCAGGAGTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                               /transl_table=11
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                                                                                                                                                     member"
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Pred. No. 4e-
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7438. .8277
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al Similarity 53.8%;
432; Conservative
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Matches 43
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                                                                                                                                                                                                                                                                                                                                                QHLSKILIKESAANTVEVFGLKKDLLNDLLTGIKDNTNFNIKYNPYYENNRLGFSGIF
GYYYNKNFR ESELSYETFHIKNNGYKRIDCEKHFALAKEISGSNNPANNKYVTLIN
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SIGIKFIL"
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LATTWDTKHPHQSAEDKYYYMWTGITLSPFIINACYDFILKKTRNVAPYLCLGVGGN
FIDFLDQVSFKRAYQARVGISFPVSPNIAFFIDGSFHGHLNNQFSDLPVYDYSSSGFP
TISAKFNANFLTSSIGIRFIS"
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                                                                                  319 TIT---AGGGIACAAITIGAAGGIICTIAIGAGAAITITIGAACCTGAAAGACAATGGIAC 375
7771 AGICTAAGACTIGAAGGIICTIACGAAAAITIGAIGICAAAGACTIGAAGACTIGAAGGIICTIACGAAAAITIGAIGICAAAGACTIGAAGACTI
                                                                                                                                                                    7831 TACTCAGCAAAAGATGCTTTTAGGTTTTTTGCTCTAGCACGTAATACGTCTACTACTGTT 7890
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                                                                                                                                                                                                                                                                                                                                                                                                                                  726
                             259 CCTACTTATGCAAGCAGTTTTGCAGGGTTTAGTGGTATCATTGGATATTATGTTAATGAC 318
                                                                                                                                           376 CCTGAGAATAGCCAAAGCTACAAATTTTTTGCTTTGTCTCGAAATGCTACAAATAGTGAT 435
                                                                                                                                                                                                 436 AAT-----AAGITTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCTTAAT 486
                                                                                                                                                                                                                                                                                                                  547 GGTGTTGGTGCAGATTATATATAAAGTTTTTAGGTATATCATTGCCTAAGTTTTCTTATCAA
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December 28, 2005, 10:46:11; Search time 620 Seconds (without alignments) 8739.347 Million cell updates/sec Run on:

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1 atgaattacaaaagatttgt.......ttggatttagatttgcgcta 813 Title: Perfect score: Sequence:

Scoring table:

4996997 segs, 3332346308 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_21:\* Database :

geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2004as: \* geneseqn2004bs: \* geneseqn2003cs:\* geneseqn2003ds:\* genesegn1980s:\*genesegn2000s:\* geneseqn2003bs:\* geneseqn2003as:\* ;; 10

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesegn2005s:\*

SUMMARIES

Regult		One re				
NO.	Score	Match	Match Length DB	DB	ID	Description
1	813	100.0	813	9	ABK68878	Abk68878 DNA encod
7	162.2	20.0	840	0	AAX34754	Aax34754 DNA encod
٣	162.2	20.0	840	9	ABS63287	Abs63287 DNA encod
4	162.2	20.0	840	σ	ADA09756	Ada09756 E. chaffe
ហ	162.2	20.0	840	14	ADW04249	Adw04249 Erlichia
9	150.8	18.5	852	7	AAX34755	Aax34755 DNA encod
7	150.8	18.5	852	ø	ABS63288	Abs63288 DNA encod
80	150.8	18.5	852	6	ADA09758	Ada09758 E. chaffe
6	150.8	18.5	852	14	ADW04251	Adw04251 Erlichia
10	147.2	18.1	840	9	ABK68876	Abk68876 DNA encod
11	147.2	18.1	843	9	ABS63299	Abs63299 DNA encod
12	147.2	18.1	843	6	ADA09780	Ada09780 E. canis
13	147.2	18.1	843	14	ADW04273	Adw04273 Ehrlichia
14	146.6	18.0	726	9	ABS63306	Abs63306 DNA encod
15	146.6	18.0	726	σ	ADA09794	Ada09794 E. canis
16	146.6	18.0	726	14	ADW04287	Adw04287 Ehrlichia
17	146.4	18.0	849	9	ABT11835	Abt11835 E chaffee
18	146.4	18.0	849	14	AEB95350	Aeb95350 Ehrlichi

	Abs63289 DNA encod	Ada09760 E. chaffe	Adw04253 Erlichia	Abs63305 DNA encod	Ada09792 E. canis	Adw04285 Ehrlichia	Aax34745 DNA encod	Ö	ш	Adw04231 Erlichia				Ada09742 E. chaffe	Adw04235 Erlichia			Aav07179 Ehrlichia	Aax34759 DNA encod	Abs63291 DNA encod	ш	Adw04257 Ehrlichia		Aac68705 Ehrlichia	DNA	Ada09744 E. chaffe	
	6 ABS63289	9 ADA09760	14 ADW04253	6 ABS63305	) 9 ADA09792	) 14 ADW04285	1 2 AAX34745	6 ABS63278	•	1 14 ADW04231		7 3 AAC68704	-	7 9 ADA09742	7 14 ADW04235	3 4 AAS07578	3 3 AAC68716	3 2 AAV07179	7 2 AAX34759	7 6 ABS63291	7 9 ADA09764		3 2 AAX34748		3 6 ABS63281	3 9 ADA09744	
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### ALIGNMENTS

Ehrlichia canis infection; vaccine; serodiagnostic; gene; p28; ss; DNA encoding Ehrlichia canis p28-9. BP. Walker DH, Yu X, Mcbride JW; 12-SEP-2001; 2001WO-US028759. 12-SEP-2000; 2000US-00660587 ABK68878 standard; DNA; 813 (first entry) (RERE-) RES DEV FOUND WPI; 2002-351882/38. P-PSDB; AAU96118. Ehrlichia canis. WO200222782-A2. antibacterial. 02-JUL-2002 21-MAR-2002. ABK68878; RESULT 1 ABK6887 

New recombinant homologous 28 kilodalton immunodominant protein Ehrlichia canis, useful for treating Ehrlichia canis infections. Claim 5; Fig 16; 106pp; English.

from

The invention relates to a recombinant homologous 28 kDa immunodominant protein, P28 (1) of Ehrlichia canis. (1), a 28-kDa antigen preferably dispersed in a pharmaceutically acceptable carrier, is useful for inhibiting B. canis infection in a subject. (1) is useful in the development of vaccines and serodiagnostics that are particularly effective for disease prevention and serodiagnosis. ABK68852-ABK68878 represent the 28-kDa antigen coding sequences and PCR primers of the

Aax34756 DNA encod

AAX34756

N

828

16.6

135

P30;

canis;

N

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142 AATTTTAGTAATTTTTCAGCTGAAGAAACAATTCCTGGTATTACAAAAAAGATTTTTGCG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAGIGGGTCTTCTATCGATCCTAACACTTATTCAAACTTTCAAGGTCCATATACT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTACTTATGCAAGCAGTTTTGCAGGTTTTAGTGGTATCATTGGATATTATGTTAATGAC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 GTTACATTTCAAGATAATGCTGCTAGTTTCAGTGGAGCAATTGGATATTCTTACCCCGAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AGICTAAGACITGAACITIGAAGGITCITACGAAAATITICATGTCAAAGATCCTAAAGAC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT-----AAGTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCTTTAAT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGATGCTCAAAAATATACAGTTATGAAGAATAATGGCTTATCTGTTGCATCATCATG 513
                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAX06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAX06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 AATTITICIGAAGGGAGGAGAGCTITATATATAGGTAGTCAGTATAAAGTTGGTATTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GTAGGTGTTACGCTGAGTACATTTGTTTTTTTTTTTTGTGGTGCTTTTTTCTGATGCA
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                                                                                                                                                                                                                                                                                                                                        Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 840 BP; 279 A; 128 C; 136 G; 297 T; 0 U; 0 Other;
                                            Ehrlichia chafeensis; E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 20.0%; Score 162.2; DB 2; al Similarity 53.8%; Pred. No. 2.1e-28; 432; Conservative 0; Mismatches 353;
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 14A; 55pp; English
                                            OMP;
                                                                                                                                                                            98WO-US019600
                                                                                                                                                                                                         97US-0059353P
               DNA encoding OMP-1V protein
                                          Outer membrane protein;
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                                                                                       Ehrlichia chaffeensis.
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Best Local Similarity
Matches 432; Conserv
                                                                                                                                                                                                                                                                                                             P-PSDB; AAY06954
                                                           detection; dog;
                                                                                                                                                                                                         19-SEP-1997;
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                                                                                                                                               25-MAR-1999
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                                                          Length 813;
                             T; 0 U; 0 Other;
                                                                                     Indels
                                                       Query Match 100.0%; Score 813; DB 6; I Best Local Similarity 100.0%; Pred. No. 4.1e-182; Matches 813; Conservative 0; Mismatches 0;
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                             Sequence 813 BP;
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05-JUL-1999
 invention
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141 153

93

Gaps

18;

Indels

Length 840;

Ehrlichia

453

435

153

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The invention relates to an isolated polynucleotide encoding an outer membrane protein (OMP) of Bhrlichia canis or Bhrlichia chaffeensis used the the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the serum sample and the polypeptide, where formation of a complex is indicative of infection with B. chaffeensis. This sequence represents DNA encoding an Bhrlichia outer membrane protein
546
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                                                                                                                          GGANAACTAGGTATTAGTTATTACTTCTTTCCTAAGATTAATGTATTTGCTGGTGGGTAC 693
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                 GTTAAGTTTGGTGTCAACTACCCTCTAAATGTTAATACTATGTTGTTTGGTGGGGGTTAT
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726 750 786 810

Sequence 840 BP; 279 A; 128 C; 136 G; 297 T; 0 U; 0 Other;

invention

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          394 TACTCAGCAAAAGATGCTTTTTAGGTTTTTTTGCTCTAGCACGTAATACGTCTACTACTGTTT 453
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                                                                                                                                                                                                                                                                                                                    GGAAAACTAGGTATTAGTTACTTCTTTCCTAAGATTAATGTATTTGCTGGTGGGTAC
                                              AAT-----AAGTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCTCTTAAT
                                                                                                                                                              514 ATCAATGGTTGTTATGATCTATCTTTTAATAATTTAGTCGTATCACCTTATATATGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATCTGACGTTCCTAGAACTACTTCAGCTTCTGCTACTTTAAATACTGATTATTTTGGT
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19-MAY-1999; 99US-00314701.
28-JAN-2002; 2002US-00059964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        purification; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-064871/07
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OHASHI N.
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(OHAS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polynucleotide encoding a variant of the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer membrane protein of E. canis, or an antigenic fragment of the E. canis P30 protein, or comprising a sequence which is the complement of canis and E. chaffeensis outer membrane proteins and their encoding nucleic acids. The polynucleotide 672 of ADA09764. Also disclosed are E. chaffeensis outer membrane proteins and their encoding nucleic acids. The polynucleotides are useful for producing E. chaffeensis outer membrane protein, for designing hybridiation probes for isolating and identifying cDNA and genomic clones encoding the OMP) or its allelic forms, for designing primers for PCR. The polypeptides encoded by the polynucleotide is useful for diagnosing human ehrlichiosis sequence encodes an E. chaffeensis outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTACTTATGCAAGCAGTTTTGCAGGGTTTAGTGGTATCATTGGATATTATGTTAATGAC 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 AATTITAGTAATTITTCAGCTGAAGAAACAATTCCTGGTATTACAAAAAAGATTTTTGCG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTTTTCTGAAGGGAGGAGGACTTTATATATACGTAGTCAGTATAAAGTTGGTATTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide encoding outer membrane protein P30 of Ehrlichia canis or its variant or fragment, useful for producing Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 840 BP; 279 A; 128 C; 136 G; 297 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
monocytic ehrlichiosis; Rocky Mountian spotted fever; canine ehrlichiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.0%; Score 162.2; DB 9;
53.8%; Pred. No. 2.1e-28;
tive 0; Mismatches 353;
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                                                                                                                                                                                99US-00314701
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                                                                                                                                                                                                                                                                                                Ohashi N;
                                                                Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                     WPI; 2003-553952/52
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Best Local Similarity
Marches 432; Conserv
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                                                                                                    JS6544517-B1
                                                                                                                                                                                19-MAY-1999;
                                                                                                                                                                                                                      18-SEP-1998;
                                                                                                                                          08-APR-2003
                                                                                                                                                                                                                                                                                                Rikihisa Y,
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                                                                                                                                   The invention relates to nucleic acid sequences encoding outer membrane proteins (OMP) of Erlichia chaffeensis (designated as OMP proteins) and Ehrlichia canis (designated as P30F proteins). The OMP polynucleotide is useful in preparing a composition for diagnosing, treating or preventing an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present sequence is the Erlichia chaffeensis OMP DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATCTGACGTTCCTAGAACTACTTCAGCTTCTGCTACATTAAATACTGATTATTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        751 cirgaigaarircciaaagcaacircigcagragciacaciraargrigcriairirggr
                              New polynucleotide encoding an outer membrane protein (OMP) of Ehrlich canis or Ehrlichia chaffeensis, useful in preparing a composition for diagnosing or preventing E. canis or E. chaffeensis infection.
                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                               DB 14; Length 840;
                                                                                                                                                                                                                                                             Sequence 840 BP; 279 A; 128 C; 136 G; 297 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                0; Mismatches 353; Indels
                                                                                                                                                                                                                                                                                              Score 162.2; DB 1.
Pred. No. 2.1e-28;
                                                                                                    SEQ ID NO 23; 122pp; English
                                                                                                                                                                                                                                                                                            20.0%;
53.8%;
                                                                                                                                                                                                                                                                                                                                Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                Local Similarity
P-PSDB; ADW04250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547
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                                                                                                      Claim 7;
                                                                                                                                                                                                                                                                                                 Query Match
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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 AGAATTTGAAGGTTCTTATGAGAATTTTGAACCTGAAAGACAATGGTACCCTGAGAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGAGAGGACTTTATATAGGTAGTCAGTATAAAGTTGGTATTCCCAATTTTAGTAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 Grecacresecraratercasresacarataraaccracrerrerecertrasraatrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 AAGCAGTTTTGCAGGGTTTAGTGGTATCATTGGATATTATGTTAATGACTTT---AGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 AGATAATGCTGTTAGCTTCAGTGCAGCTGTTGGATATATTTCCCCAAGACAGTCCAAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      membrane protein; OMP; Ehrlichia chafeensis; E. canis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 852 BP; 295 A; 115 C; 141 G; 301 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 150.8; DB 2; Length
Pred. No. 1e-25;
0; Mismatches 307; Indels
809
                                                    833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 15A; 55pp; English
  TGGGAGATTGGATTTAGATTTGC
                                              811 GGTGAAGCTGGAGTAAAGTTTAC
                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0059353P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.5%;
54.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US019600
                                                                                                                                                                                                                                                                                                                                                                       DNA encoding OMP-1W protein.
                                                                                                                                                                                     852
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity 54.6
402; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                     AAX34755 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rikihisa Y, Ohashi N;
                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-254290/21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; dog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9913720-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-1997;
                                                                                                                                                                                                                                                                                        27-AUG-2003
05-JUL-1999
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Best Local 8
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patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the serum sample and the polypeptide, where formation of a complex is indicative of infection with E. chaffeensis. This sequence represents DNA encoding an Ehrlichia outer membrane protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAGGICATAGGAAATAAAATTTAACAATTTAAATGTTCAACACGTTGTTAGTCTTAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by providing a serum sample from
                                                                                                                                                                                                                                                            |||||
TTCACTTAAAGAAACTTATACTGACACTAAAGAGTTATTAGGACTAGCAAAAGATATTAA
                                                                                                                                                                                                                                                                                            GTCT-----GAGATAAATACTCACAGCAATTTTACACGATCATATGACCCTACTTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAGGTTGTAGGTGATAGGCATGAGAGAGTAGAAATAGCTTACCATCCTACTGCATTATC
                                                                                                                                                                                                                GTGCACTGGGCTATATGTCAGTGGACAATATAAACCTACTGTTTCTCACTTTAGTAATTT
                                                                                                                                                                                                                                         TTCAGCTGAAGAAACAATTCCTGGTATTACAAAAAAGATTTTTGCGTTAGGTCTTGATAA
                                                                                                                                                                                                                                                                                                                    GTCTATTACAGATATAACAACAATAAAAATTCAACATTCCTTATAACACAAAATTTCA
                                                                                                                                                                                                                                                                                                                                                                                                    AGAATTTGAAGGTTCTTATGAGAATTTTTGAACCTGAAAGACAATGGTACCCTGAGAATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AATAAGTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCTCTTAATGTAAA
                                                                                                                                                            Gaps
                                                                                                                                                          27;
                                                                                                                                Length 852;
                                                                                                       Sequence 852 BP; 295 A; 115 C; 141 G; 301 T; 0 U; 0 Other;
                                                                                                                                                            Indels
                                                                                                                                 Score 150.8; DB 6;
Pred. No. 1e-25;
0; Mismatches 307;
                                                                                                                                Score 150.8;
Pred. No. 1e-
  ehrlichiosis can be diagnosed
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                                                                                                                                                          Conservative
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                                                                                                                                               Local Similarity
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AC ADA09758;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used in the diagnosis of infection. An infection such as human ehrlichiosis o
TGAGGTAGAATGGTCTTATGAAGAATTTGACGTTAAAAATCCTGGTAATTACGTAGTAAG
                                                                                                                                                                                                                                                                                            TAAGGTTGTAGGTGATAGGCATGAGAGTAGAAATAGCTTACCATCCTACTGCATTATC
                                                                                                                                                                                                         TGGTGGGGACATTATAGAATTTTTTAGTGCTGTAAGTTTTAAATTTGCTTATCAAGGTAA
                                                                                                                                                                                                                                                                                                                                                              TCA---TCCTAAGTCTACTTTTGCAGTAGCTACTCTTAATGTTGAGTATTTCGGTAGTGA
                                                                                                                                                                                                                                                                GGTAGGTATCAGTTATCTCTCTAATATGATTATATTTTGCTGACGGATATTACCA
                                                                                                                                                                                                                                                                                                                     TAAGGICATAGGAAATAAATTTTAAATGTTCAACACGCTTGTTAGTCTTAACAG
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                                                                                                      TGGTGCAGATTATATAAAGTTTTTAGGTATATCATTGCCTAAGTTTTCTTATCAAGTTAA
                                                                                                                                                                                                                                        TGAAGCCTTCAGGTATATTGCTTTAGCAAGAGGAATTGATAATCTTCAAAAATATCCTGA
                                                                             ----AATAAGTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCTCTTAATGTAAA
                                                                                                                                 ehrlichiosis; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding Bhrlichia chaffeensis outer membrane protein (OMP) #13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       벙
                          CCAAAGCTACAAATTTTTTGCTTTGTCTCGAAATGCTACAAATAGTGAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outer membrane of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds; P30F;
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the diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purification; diagnosis; outer membrane protein; OMP; P30F protein;
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                                                                                                                                                                                                                                              ----AATAAGTTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCTCTTAATGTAAA
                                                                                                                                           471 AACAAATAAGTATGTTGTTATAAAGAACAATGGCTTATCTGTCGCATCCATTATAATCAA
                                                                                                                                                                                                                                                                                                                       TGGTGCAGATTATATAAAGTTTTTAGGTATATCATTGCCTAAGTTTTCTTATCAAGTTAA
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/product= "Erlichia chaffeensis mature OMP protein"
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19-MAY-1999; 99US-00314701.
28-JAN-2002; 2002US-00059964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polynucleotide encoding a variant of the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer membrane protein of E. Canis, or an antigenic fragment of the E. Canis p30 protein, or comprising a sequence which is the complement of nucleotide 99 through nucleotide 672 of ADA09764. Also disclosed are E. canis and B. chaffeensis outer membrane proteins and their encoding nucleic acids. The polynucleotides are useful for producing E. canis or E. chaffeensis outer membrane protein, for designing hybridisation probes for isolating and identifying CDNA and genomic clones encoding the OMP) or its allelic forms, for designing primers for PCR. The polympeptides encoded by the polynucleotide is useful for diagnosing human ehrlichiosis (Rocky mountain spotted fever) or canine ehrlichiosis. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bhrlichia canis or its variant or fragment, useful for producing Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins
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Pred. No. 1e-25;
0; Mismatches 307; Indels 27
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                                                               chaffeensis DNA encoding outer membrane protein OMP-1W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence encodes an E. chaffeensis outer membrane protein
                                                                                                                     ds; gene; outer membrane protein; circulating leukocyte; monocytic ehrlichiosis; Rocky Mountian spotted fever; canine ehrlichiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosing and treating ehrlichiosis.
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P-PSDB; ADA09759.
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Matches 402;
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                                                                                                        The invention relates to nucleic acid sequences encoding outer membrane proteins (OMP) of Erlichia chaffeensis (designated as OMP proteins) and Ehrlichia canis (designated as P30F proteins). The OMP polynucleotide is useful in preparing a composition for diagnosing, treating or preventing an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present sequence is the Erlichia chaffeensis OMP DNA.
                                  New polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis, useful in preparing a composition for diagnosing or preventing E. canis or E. chaffeensis infection.
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                                                                                                                                                                                                                   DB 14; Length 852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 CCAAAGCTACAAATTTTTTGCTTTGTCTCGAAATGCTACAAATAGTGAT--
                                                                                                                                                                                             852 BP; 295 A; 115 C; 141 G; 301 T; 0 U; 0 Other;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                               Pred. No. 1e-25;
0; Mismatches 307;
                                                                                                                                                                                                                  Query Match 18.5%; Score 150.8; Best Local Similarity 54.6%; Pred. No. 1e-Matches 402; Conservative 0; Mismatches
                                                                                   Claim 7; SEQ ID NO 25; 122pp; English
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WPI; 2005-064871/07
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GATGGTGCTTTTTCTGA-----TGCAAATTTTTCTGAAGGGAGGAGAGCACTTTAT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a recombinant homologous 28 kba immunodominant protein, p28 (T) of Ehrlichia cannis. (I), a 28-kba antigen preferably dispersed in a pharmaceutically acceptable carrier, is useful for inhibiting E. canis infection in a subject. (I) is useful in the development of vaccines and serodiagnostics that are particularly effective for disease prevention and serodiagnosis. ABK68852-ABK68978 represent the 28-kba antigen coding sequences and PCR primers of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 raicagróririgoagarcorgraggircaágaacraargaraacaaagaággorrorac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant homologous 28 kilodalton immunodominant protein from
Ehrlichia canis, useful for treating Ehrlichia canis infections.
                                                                                                                                                                                                                                 88;
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                                                                                                                                                                                                                              Shrlichia canis infection; vaccine; serodiagnostic; gene; p28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 840 BP; 301 A; 141 C; 144 G; 254 T; 0 U; 0 Other;
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Pred. No. 7.4e-25;
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Mismatches 358;
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53.2%;
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ABK68876 standard; DNA; 840
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Best Local Similarity 53.2<sup>3</sup>
Matches 445; Conservative
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                                                                                                                                                                                                                                                            antibacterial.
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in the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the serum sample and the polypeptide, where formation of a complex is indicative of infection with E. chaffeensis. This sequence represents DNA encoding an Ehrlichia outer membrane protein
                                                                                                                                                                                                                                                                   -TGCAAATTTTTCTGAAGGGAGGAGGAGGACTTTAT
                                                                                                                                                                                                                                                                                             TATCAGTCTTTTGCAGATCCTGTAGGTTCAAGAACTAATGATAACAAAGAAGGCTTCTAC
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                                                                                                                             Sequence 843 BP; 303 A; 141 C; 144 G; 255 T; 0 U; 0 Other;
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Pred. No. 7.4e-25;
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53.2%;
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                                                                                                                                                                                                                AGTGGTAGTATTCCTTTAGCACCTTATATGTGTGCTGGTGTTGGTGCAGATTATATAAAAG
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                           ararcaddarirircaddaagararrddriacrcrargaacaagaaradaacrrdaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polynucleotide encoding a variant of the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer membrane protein of E. canis, or an antigenic fragment of the E. canis P30 protein, or comprising a sequence which is the complement of canis ancleotide 99 through nucleotide 672 of ADA09764. Also disclosed are E. canis and E. chaffeensis outer membrane proteins and their encoding nucleic acids. The polynucleotides are useful for producing E. chaffeensis outer membrane protein, for designing hybridiation probes for isolating and identifying cDNA and genomic clones encoding the OMP) or its allalic forms, for designing primers for PCR. The polypeptides encoded by the polynucleotide is useful for diagnosing human ehrlichiosis sequence encodes an E. canis outer membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynuclectide encoding outer membrane protein P30 of Ehrlichia canis or its variant or fragment, useful for producing Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins for Baragnosing and treating ehrlichiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                outer membrane protein; circulating leukocyte; ehrlichiosis; Rocky Mountian spotted fever;
                                                                                                                                                       canis DNA encoding outer membrane protein p30-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.1%; Score 147.2; DB 9; 53.2%; Pred. No. 7.4e-25; ive 0; Mismatches 358;
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                      ADA09780 standard; DNA; 843
                                                                                                           (first entry)
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Best Local Similarity 53.2
Matches 445; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohashi N;
                                                                                                                                                                                                                                            canine ehrlichiosis.
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                                                                                                                                                                                                                                                                                       Ehrlichia canis
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                                                                                                           06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                              08-APR-2003
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The invention relates to an isolated polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeenais used in the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the serum sample and the polypeptide, where formation of a complex is indicative of infection with E. chaffeensis. This sequence represents DNA encoding an Ehrlichia outer membrane protein
                                         661 Arcaccagaagrerergearrratigergaracraccargecerratigeraraaa 720
                                                                                                         721 TTTGAGAAGATACCTGTA---ATAACTCCTGTAGTATTAAATGATGCTCCTCAAACCACA 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 GAAACAATTCCTGGTATTACAAAAAGATTTTTGCGTTAGGTCTTGATAAGTCTGAGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 GAGGCATTGTTTGGGCTAAAACAAGATATTAGTTCTATTTTACGTAATAAAGAGACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 AATACTCACAGCAATTTTACACGATCATATGACCCTACTTATGCAAGCAGTTTTGCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 CAATATAATAACAATTTTAACGTTCCCTATACTGCAAAATTTCAAGACGACTTTGCGAGT
          CTAAATGTTAATACTATGTTGTTGGTGGGGGTTATTACCATAAGGTTGTAGGTGATAGG
                                                                          CATGAGAGAGAGAAATAGCTTACCATCCTACTGCATTATCTGACGTTCCTAGAACTACT
                                                                                                                                                                                                                                                                                                                                                                                          Outer membrane protein; OMP; gene; ds; P30F; ehrlichiosis; infection.
                                                                                                                                         TCAGCTTCTGCTACTTAAATACTGATTATTTTGGTTGGGAGATTGGATTTAGATT
                                                                                                                                                                          rcrecrrcagradcrerrgacgriggaracririggeggagaaarrggaargaggri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polynucleotide encoding an outer membrane protein of S.chaffeensis used in the diagnosis of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 726;
                                                                                                                                                                                                                                                                                                                                                             DNA encoding Ehrlichia canis outer membrane protein (P30F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 726 BP; 255 A; 99 C; 112 G; 260 T; 0 U; 0 Other;
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Pred. No. 9.8e-25;
0; Mismatches 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 32A; 49pp; English
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54.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171
                                                                                                                                                                                                                                                                              The invention relates to nucleic acid sequences encoding outer membrane proteins (OMP) of Erlichia chaffeensis (designated as OMP proteins) and Ehrlichia canis (designated as P30F proteins). The OMP polynucleotide is useful in preparing a composition for diagnosing, tracting or preventing an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                             New polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis, useful in preparing a composition for diagnosing or preventing E. canis or E. chaffeensis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 147.2; DB 14; Length 843; Pred. No. 7.4e-25; 0; Mismatches 358; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 843 BP; 303 A; 141 C; 144 G; 255 T; 0 U; 0 Other;
                                                                                                                                                                                                  canis or Ehrlichia chaffeensis, useful i
diagnosing or preventing E. canis or E.
                                                                                                                                                                                                                                                                                                                                                                  sequence is the Erlichia canis P30F DNA.
                                                                                                                                                                                                                                                 Claim 2; SEQ ID NO 47; 122pp; English.
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53.2%;
19-MAY-1999; 99US-00314701.
28-JAN-2002; 2002US-00059964.
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                                                                                                                                 WPI; 2005-064871/07.
                                                                                              Ohashi
                                            RIKIHISA Y.
OHASHI N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                              Rikihisa Y,
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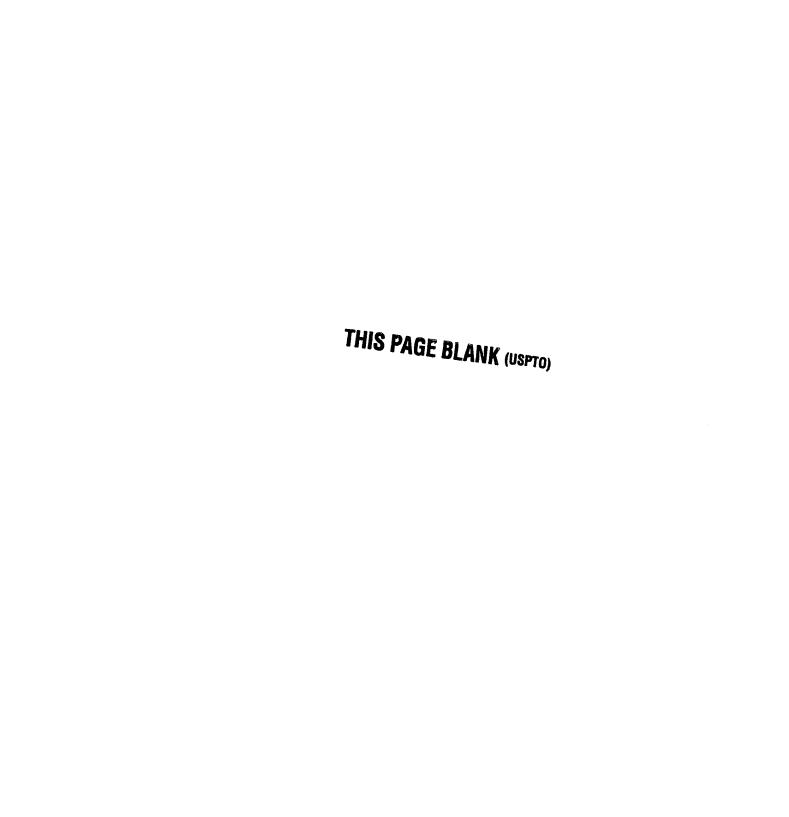
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TTTAGTGGTATCATTGGATATTATGTT----AATGACTTTAGGGTAGAATTTGAAGGTTCT
                     TTCAGCATAGCTGTTGGATATTTGCTAACAATGGTCCAAGAATTGAAATAGAAGGATCT
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monocytic ehrlichiosis; Rocky Mountian spotted fever;
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P-PSDB; ADA09795.
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                                                                                                                   The invention relates to an isolated polynucleotide encoding a variant of the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer membrane protein of E. canis, or an antigenic fragment of the E. canis P30 protein, or comprising a sequence which is the complement of nucleotide 99 through nucleotide 672 of ADA09764. Also disclosed are E. canis and E. chaffeennis outer membrane protein and their encoding nucleic acids. The polynucleotides are useful for producing E. canis or E. chaffeensis outer membrane protein, for designing hybridisation probes for isolating and identifying cDNA and genomic clones encoding the OMP) or its allelic forms, for designing primers for PCR. The polypeptides encoded by the polynucleotide is useful for diagnosing human ehrlichiosis (Rocky mountain spotted fever) or canine ehrlichiosis. The present
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New isolated polynucleotide encoding outer membrane protein P30 o
Bhrlichia canis or its variant or fragment, useful for producing
Ehrlichia canis or Bhrlichia chaffeensis outer membrane proteins
diagnosing and treating ehrlichiosis.
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 726;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 726 BP; 255 A; 99 C; 112 G; 260 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                    sequence encodes an E. canis outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                      Score 146.6; DB 9;
Pred. No. 9.8e-25;
0; Mismatches 284;
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                                                                                     Disclosure; Fig 32; 105pp; English
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54.0%;
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Best Local Similarity
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Search completed: December 28, 2005, 10:56:44 Job time : 626 secs



# Thu Dec 29 08:14:04 2005

OM micletc - mi	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM mucleic - mucleic search, using sw model
Run on:	
Title: Perfect score:	9412.375 Million cell updateB/Bec US-10-731-554-45 B13
Sequence:	
Scoring table:	IDENTITY NUC Gapop 10.0, Gapext 1.0
Searched:	41078325 segs, 23393541228 residues
Total number of	Total number of hits satisfying chosen parameters: 82156650
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1: 9b est1:\*
2: 9b est2:\*
4: 9b est3:\*
5: 9b est5:\*
6: 9b est5:\*
7: 9b est6:\*
8: 9b est6:\*
1: 9b gss1:\*
11: 9b gss2:\*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

EST: \*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	AL063921 Drosophil	AL098379 Drosophil	BX173672 Danio rer	AL069706 Drosophil	AL069797 Drosophil	AL068607 Drosophil	CK573092 1099 Plas	AL078714 Drosophil	AL098845 Drosophil	BX152436 Danio rer		CW973509 AIAA-aaa5	AL101513 Drosophil	CG807194 1118078H0	BZ388480 EINDL21TF	CG803197 1118039H0	BW073695 BW073695	BW143210 BW143210	AZ549806 ENTFL24TR	AL075933 Drosophil	AQ946120 Sheared D	AL070972 Drosophil
SUMMARIES		QI	CNS0039G	CNS0100X	BX173672	CNSOOEVL	CNSOOESI	CNS00LO0	CK573092	CNS00LT2	CNS010DV	BX152436	BX139987	CW973509	CNS012FZ	CG807194	BZ388480	CG803197	BW073695	BW143210	AZ549806	CNS00J4X	AQ946120	CNSOOFMC
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		Score	62.8	60.8	56.8	56.4	55.8	54.2	54	53	52.6	51.2	51	51	50.4	50.2	20	49.8	49.6	49.6	49.6	49.4	49.2	49.2
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## ALIGNMENTS

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d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/clone="BACN03G04"
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Submitted (23-UTL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melannogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre
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   Length 1101;
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llarity 15.8%; Pred. No. 0.00051;
Conservative 272; Mismatches 270;
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                                                                                      Humphray, S.J., Huckle, B. and Durham, J.L.
Direct Submission
Submitted (13.9Mar.2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 150M6. 150M6 is part of the Danlokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Statinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 829)
                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTACAAAAAATTTTTGCGTTAGGTCTTGATAAGTCTGAGATAAATACTCACAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAAGACAATGGTACCCTGAGAATAGCCAAAGCTACAAATTTTTTGCTTTGTCTCGAAA
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                                                                                                                                                                                                                                                                                                                        DB 10; Length 829;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                       Score 56.8; DB 10;
Pred. No. 0.013;
0; Mismatches 312;
                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
                                                                                                                                                                                                                                                           /clone="DKBY-150M6"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                          organism="Danio rerio"
 GI:28005377
           GSS.
Danio rerio (zebrafish)
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VERSION
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                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                 REPERENCE
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Genoecope.

By 1919 (SYRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Gollaboration with the Barkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-99 and was constructed by partial Ecost digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

Location/Qualifiers
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CNSGOBUL 1101 bp DNA linear GSS 04-JUN-19 Drosophila melanogaster genome survey sequence T7 end of BAC: BAC23B23 of RPCI-98 library from Drosophila melanogaster (fruit £1y), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 ATTATGTTAATGACTTTAGGGTAGAATTTGAAGGTTCTTATGAGAATTTTGAACCTGAAA
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                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 6.9%; Score 56.4; DB 10; Length al Similarity 32.1%; Pred. No. 0.016; 208; Conservative 113; Mismatches 320; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29823"
                                                                                                                                                                                                      (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                            Drosophila melanogaster
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요 ò 유 ઠે 유

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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kastucyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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Burvey sequence TET3 end of BAC:
rom Drosophila melanogaster (fruit
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                                 TCTCGAAATGCTACAAATAGTGATAATAAGTTTATAGTACTAGAGAATAACGGCGTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACAAGTCTCTTAATGTAAATGTTTGTTATGATATTGCTAGTGGTAGTATTCCTTTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   532 CCTTATATGTGTGCTGGTGTTGGTGCAGATTATATAAAAGTTTTTAGGTATATCATTGCCT
                                                                                             175 CCTGGTATTACAAAAAAGATTTTTGCGTTAGGTCTTGATAAGTCTGAGATAAATACTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGWRDGXKGKKRGTGAAATRAARVGWKAKTKADWWDHTTTWTKKWKTTTTKDRWTTKTGTG
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                                                                                                                                                                                                                                  918 TKTTWKWTGWATGGWGAGAAGKAGWGGWGRWGWDAGTRWGWRKADTDKGKWDTGWGKTGT
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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BACR32D23 of RPCI-98 library from
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SOURCE
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29115 of RPCI-98 library from Drosophila melanogaster (fruit AL069797)
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                       484
                                                                                                                                                                                                                                                        CTGGTGTTGGTGCAGATTATAAAGTTTTTAGGTATATCATTGCCTAAGTTTTCTTATC 604
ATGTAAATGTTTGTTATGATATTGCTAGTGGTAGTATTCCTTTAGCACCTTATATGTGTG
                                                                                                                                                                                            CAAATAGTGATAATAAGTTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCTCTTA
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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6.9%; Score 55.8; DB 10;
Best Local Similarity 21.6%; Pred. No. 0.023;
Matches 138; Conservative 206; Mismatches 292;
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/db_xref="taxon:7227"
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/clone_lib="RPCI-98
/note="end : TET3"
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Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                /notes "Vector: pTriplEx2; Plasmodium yoelii liver stage parasites were harvested by laser capture microdissection, from infected Balb/C mouse liver cryosections, 40 hours after incoulation with sporozoites. Total RNA was then isolated using the StrataPrep Total RNA microprep Kit from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 TGATAAGTCTGAGATAAATACTCACAGCAATTTTACACGATCATATGACCCTACTTATGC 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 ATTTGAAGGTTCTTATGAGAATTTTGAACCTGAAAGACAATGGTACCCTGAGAATAGCCA 389

    - Web : www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 TCATAATAAATCTTATAATTACGATAATACAAATAGCAACAATCATGAAAATAATAATGC
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/dev_stage="40 hour liver schizont"
/clone_lib="Plasmodium yoelii liver stage LCM cDNA
library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 7; Length 530;
Pred. No. 0.055;
0; Mismatches 195; Indels
                                                                                                              /organism="Plasmodium yoelii"
/mol_type="mRNA"
/gtrain="17X NL"
      Email: jsacc001@umaryland.edu
                                                             Location/Qualifiers
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Best Local Similarity 46.7%;
Matches 171; Conservative
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
I (bases 1 to 530)
Saccij,JB. Jr., Ribeiro,J.M.C., Huang,F., Alam,U., Russell,J.A.,
Blair,P.L., Witney,A., Carucci,D.J., Azad,A.F. and Aguiar,J.C.
Transcriptional analysis of in vivo Plasmodium yoelii liver stage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGTTCTTATGAGAATTTTGAACCTGAAAGACAATGGTACCCTGAGAATAGCCAAAGCT
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University of Maryland School of Medicine
BRB 13-009, 655 W. Baltimore Street, Baltimore, MD 21201, USA
Tel: 410 706 4071
                                             can
and how to order individual BAC clones, the entire library, filters for hybridization from the BACPAC Resource Center cafound at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 1101;
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Mol. Biochem. Parasitol. 142 (2), 177-183 (2005)
15876462
Contact: Sacci JB
                                                                                                                                                           /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR32D23"
/clone lib="RRCI-98"
/note="end : TET3"
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598 TKADDTKGGKGAARG 584
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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Pear Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST librarie. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACGATCATATGACCCTACTTATGCAAGCAGTTTTGCAGGGTTTTAGTGGTATCATTGGAT 304
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                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="BACR48P19"
/clone lib="RPCI-98"
/note="end : TET3"
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CNS010DV 976 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC

CNS010DV/c LOCUS DEFINITION

RESULT

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Submitted (12-JUL-1999) Genoscope - Centre National de Sequencage: Submitted (12-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

Betermination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Hummain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 28-JAN-2003
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BACN03N21 of DrosBAC library from Drosophila melanogaster (fruit
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/plasmid="pBeloBAC11"
/note="end : SP6"
                  fly), genomic survey sequence.
AL098845
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Danio rerio
                                                            AL098845.1 GI:5610456
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/mol_type="genomic DN:
/db_xref="taxon:7955"
/clone="DKEY-99E7"
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Best Local Similarity 45.3%;
Matches 229; Conservative
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Unpublished (2004)
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Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 844)

Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submission

Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambission

Campus, Hinxton, Cambridgeshire, CB10 iSA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 9987. 9987 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
                                                                     Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 116F16. 116F16
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene, Further details:
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48.9%; Pred. No. 0.26;
ilve 0; Mismatches 143;
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Location/Qualifiers
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Location/Qualifiers
                                                                                                                                                                                                                                                         /organism="Danio rerio"
/mol_type="genomic DNA"
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/clone="DKBY-116F16"
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/note="wector pindigoBAC-536"
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Ancylostoma caninum

Ancylostoma caninum

Ancylostomatoidea; Nematoda; Chromadorea; Rhabditida; Strongylida;

Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.

I (bases 1 to 889)

Mitreva,M., McCarter,J.P., Pape,D., Ritter,E., Teagareishvili,R., Ronko,I., Wartin,J.*, Wylie,T., Dante,M., Meyer,R., Messina,D.,

Waterston,R.H., Clifton,S.W. and Wilson,R.

Genome Survey sequences from the parasitic nematode Ancylostoma
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Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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                                                                                                                     Score 51, DB 10; Length 844;
Pred. No. 0.29;
0; Mismatches 270; Indels
/tissue_type="Testis"
/note="vector pindigoBAC-536"
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Drosophila melanogaster (fruit fly)
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/note="Vector: pOTW1]"
/note="Vector: pOTW1]"
Ancylostoma caninum genomic DNA was randomly sheared, end-repaired and size fractioned to enrich for 2-4 kb fragments. Genomic DNA was provided by John Hawdon (mtminh@gwumc.edu) at George Washington University. Sequencing by Washington University Genome Sequencing Center, St. Louis, NO."
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               (mtmjmh@gwumc.edu)
          Genomic DNA provided by John Hawdon (mtmjmh@gwumc.edu
sequenced by Washington University Genome Sequencing
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Pred. No. 0.3;
 nematode@watson.wustl.edu
                                                                                                    /mol_type="genomic DNA"
/strain="Baltimore"
                                                                                      /organism="Ancylostoma
                                                                                                                               /db_xref="taxon:29170"
/dev_stage="Adult"
/lab_host="GS10"
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             6.3%;
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                                         Class: shotgun.
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GSS 26-JUL-1999

Drosophila melanogaster genome survey sequence T7 end of BAC BACN07802 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ALI01513.
ALI01513.1 GI:5613124
GSS.

DEFINITION

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ACCESSION VERSION KEYWORDS

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Direct Submission
Submitted (23-JUJ-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEDH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1094)
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/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
/clone="BACN07B02"
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/plasmId="pBeloBAC11"
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invadens genomic DNA, repairing the ends of DNA fragments with T4 Polymerase, adding BstXI adaptors and ligating into the BstXI site of a pUC-derived vector pHOS2."
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EINDL21TF EL_10_12_KB Entamoeba invadens genomic clone EINDL21.
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9712 Medical Center Drive, Rockville, MD 20850, USA
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DNA was provided by Daniel Eichinger
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Eukaryota; Entamoebidae; Entamoeba
1 (bases 1 to 670)
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Contact: Brendan Loftus
Department of Eukaryotic Genomics
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/strain="IP-1"
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Fax: 301-838-0208
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Contact: Walbot V.
Department of Biological Sciences
Stanford University
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                                   520 TCAACTACCCTCTAAATGTTAATACTATGTTGTTGGTGGGGGTTATTACCATAAGGTTG 679
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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CG807194
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Coganism="Zea mays"
(mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
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Tel: 650 723 2227
Fax: 650 725 8221
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Best Local Similarity 45.1%; Pred. No. 0.43,
Matches 187; Conservative 0; Mismatches
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Plate: 1118078 column: 2
Class: transposon_tagged.
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Walbot, V.
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COMMENT
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357 ACCTGAAAGACAATGGTACCCTGAGAATAGCCAAAGCTACAAATTTTTTGCTTTGTCTCG 416
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                                                                                                                                                                                                                                                                     237 CAATITIACACGAICAIAIGACCCIACITAIGCAAGCAGITITIGCAGGGITIAGIGGIAI 296
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177 IGGTATTACAAAAAGATTTTTGCGTTAGGTCTTGATAAGTCTGAGATAAATACTCACAG 236
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December 28, 2005, 12:15:35 ; Search time 838 Seconds (without alignments) 508.589 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                           OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SIMMARIES

		de			SUMMAKIES	
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
1	48.2	5.9	6113	9 إ	US-10-240-708-14	Sequence 14, Appl
7	45.6	2.6	20500	9	US-10-829-826B-16	16,
٣	45.6	2.6	27608	ø	US-10-829-826B-14	Sequence 14, Appl
4	45.6	5.6	27608	9	US-10-829-826B-15	Sequence 15, Appl
Ŋ	45.6	5.6	27635	9	US-10-829-826B-17	17,
9	45.2	5.6	1044	7	US-11-066-648A-1	Sequence 1, Appli
C 7	41.4	5.1	1773	9	US-10-750-185-58930	Sequence 58930, A
ω υ	41.4	5.1	139054	7	US-11-121-086-96	Sequence 96, Appl
o.	41.2	5.1	31028	9	US-10-829-826B-21	Sequence 21, Appl
10	41.2	5.1	31028	9	US-10-829-826B-22	Sequence 22, Appl
11	41.2	5.1	31028	9	US-10-829-826B-26	Sequence 26, Appl
12	41.2	5.1	31032	9	US-10-829-826B-23	Sequence 23, Appl
13	41.2	5.1	31100	9	US-10-829-826B-24	24,
14	40	4.9	6317	9	US-10-240-708-11	Sequence 11, Appl
15	39.2	4.8	1289	9	US-10-750-185-39647	Sequence 39647, A
16	39.2	4.8	9699	9	US-10-240-708-76	Sequence 76, Appl
17	39.5	4.8	27733	9	US-10-829-826B-18	Sequence 18, Appl
18	38.4	4.7	96988	7	US-11-117-187-196	Sequence 196, App
19	38	4.7	645179	9	US-10-995-561-13293	1329
20	37.8	4.6	7664	9	US-10-240-708-83	Sequence 83, Appl
c 21	37.6	4.6	159781	7	US-11-121-086-92	Sequence 92, Appl
c 55	37.6	4.6	200628	7	US-11-121-086-62	Sequence 62, Appl
c 23	37.6	4.6	207908	7	US-11-112-908-21	Sequence 21, Appl

8-74 Sequence 74, Appl	8-82 Sequence 82, Appl	Sequence 80,	8-93 Seguence 93, Appl		Sequence 35,	Sequence 29,	8-32 Sequence 32, App.	3 Seguence 43,	3 Seguence 33,	6B-19 Sequence 19, Appl	Sequence 20,	7 Sequence ·107,	5-61398 Sequence 61398,	Sequence	Sequence	.5-47268 Sequence 47268,	6-3561 Seguence 3561,	18-62 Seguence 62, Ap	8-45 Sequence 45, App]	Sequence	15-32041 Seguence 32041.
US-10-240-708-74	US-10-240-708-82	US-10-240-708-80	US-10-240-708-93	7 US-11-117-187-213	US-10-240-708-3	US-10-240-708-29	US-10-240-708-3	US-10-966-483-4	US-11-021-441-3	US-10-829-826B-19	US-10-829-826B-20	US-11-121-086-107	US-10-750-185-6	. US-10-750-185-35397	: US-10-240-708-26	. US-10-750-185-47268	. US-10-793-626-3561	. US-10-240-708-62	; US-10-240-708-45	; US-10-750-185-32418	US-10-750-185-3204
5152 6	5476 6	8961 6	10144 6	1082144	9347 6	9 9995	8093 6	9808	9808	19940 6	27528 6	197096 7	1032 6	1080	6583 6	2314 6	3803 6	6801 6	19233 6	2432 6	3330
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#### ALIGNMENTS

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Sequence 14, Application US/10240708

Sequence 14, Application US/10240708

Bublication No. UG2050282157A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

FILE REFERENCE: 5013.1012

CURRENT PAPLICATION NUMBER: US/10/240,708

CURRENT FILING DATE: 2002-10-03

PRIOR APPLICATION NUMBER: PCT/FP01/03971

PRIOR APPLICATION NUMBER: DE 10019758.8

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

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242 TTACACGATCATATGACCCTACTTATGCAAGTTTTGCAGGGTTTAGTGGTATCATTG 301

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RESULT 3
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9438 AGTGCCACCAGATAATTTAGTTACTAACAATATTGTAGCATGCCTCTATGCGGCAATTAT 9497
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                                                                                                  358 CCTGAAAGACAATGGTACCCTGAGAATAGCCAAAGCTACAAATTTTTGCTTTGTCTCGA
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APPLICANT: Bocker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Blyn Lawrence B.
APPLICANT: Hall, Thomas A.
APPLICANT: Massire, Christian
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF CORONAVIRUSES
FILE REFERENCE: IBISO075-100 (DIBIS-0058US)
CURRENT APPLICATION NUMBER: US/10/829,826B
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
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49.2%; Pred. No. 0.38;
tive 0; Mismatches 124; Indels 0;
                                GATATTATGTTAATGACTTTAGGGTAGAATTTGAAGGTTCTTATG-
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                                                                                                                                                                                                                                                                                                                                                                             TCTTATCAAGTTAAGTTTGGTGT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/10829826B Publication No. US20050266397A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
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SEQ ID NO 16
LENGTH: 20500
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9438 AGTGCCACCAGATAATTTAGTTACTAACAATATTGTAGCATGGCTCTATGCGGCAATTAT 9497
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US-10-829-826B-15

Sequence 15, Application US/10829826B

Publication No. US20050266397A1

GENERAL INFORMATION:
APPLICANT: Becker, David J.
APPLICANT: Hofstadler, Seeven A.
APPLICANT: Bampath, Rangarajan
APPLICANT: Hall, Thomas A.
APPLICANT: Hall, Thomas A.
APPLICANT: Hall, Thomas A.
APPLICANT: Hall, Lawrence B.
APPLICANT: Massire, Christian
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF CORONAVIRUSES
FILE REFRENCE: IBISO075-100 (DIBIS-0058US)
CURRENT APPLICATION NUMBER: US/10/829,826B

CURRENT FILING DATE: 2004-04-22

NUMBER OF SEQ ID NOS: 105

SEQ ID NO 15

LENGTH: 27608

TYPE: NANA
Sequence 14, Application US/10829826B
| Publication No. US20050266397A1
| GENERAL INFORMATION:
| APPLICANT: Beker, David J. |
| APPLICANT: Beker, David J. |
| APPLICANT: Bangatah, Rangarajan |
| APPLICANT: Hall, Thomas A. |
| APPLICANT: Massire, Christian |
| TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF CORONAVIRUSES |
| FILE REFERENCE: IBIS0075-100 (DIBIS-0058US) |
| CURRENT FILING DATE: 2040-04-22 |
| NUMBER OF SEQ ID NOS: 105 |
| SOFTWARE: PattsEQ for Windows Version 4.0 |
| SEQ ID NO 14 |
| LENGTH: 27608
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Pred. No. 0.42;
0; Mismatches 124; Indels
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Best Local Similarity 49.2
Matches 120; Conservative
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0; Mismatches 143; Indels
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Pred. No. 0.19;
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 58930
LENGTH: 1773
                               ; Sequence 1, Application US/11066648A; Publication No. US20050260621A1; GENEAL INFORMATION: APPLICANT: WCBKIDE, JERE W. APPLICANT: WALKER, DAVID H.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.8%;
Matches 131; Conservative
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ORGANISM: Ehrlichia canis
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US-10-750-185-58930/c
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                     JS-11-066-648A-1
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Pred. No. 0.42;
0; Mismatches 124; Indels 0;
 Length 27608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Sampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Blyn, Lawrence B.
APPLICANT: Hall, Thomas A.
APPLICANT: Hall, Thomas A.
APPLICANT: Massire, Christian
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF CORONAVIRUSES
FILE REFERENCE: IBISO075-100 (DIBIS-0058US)
CURRENT APPLICATION UNMBRR: US/10/829,826B
CURRENT FILING DATE: 2004-04-22
Score 45.6; DB 6; Length 2
Pred. No. 0.42;
0; Mismatches 124; Indels
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Publication No. US20050266397A1
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 5.6%;
 Query Match
Best Local Similarity 49.2'
Matches 120; Conservative
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Best Local Similarity 49.2
Matches 120; Conservative
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LENGTH: 27635
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US-10-829-826B-17
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82 AATTITICIGAAGGAGGAGGACTITATATATAGGTAGTCAGTATAAAGTTGGTATTCCC 141
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APPLICANT: "NALKER, DAVID H.
APPLICANT: WALKER, DAVID H.
APPLICANT: WALKER, DAVID H.
APPLICANT: WALKER, CHRISTOPHER KUYLER
TITLE OF INVENTION: AN IMMUNOREACTIVE 38 KDA FERRIC BINDING PROTEIN OF
TITLE OF INVENTION: BRILLICHIA CANIS AND USES THEREOF
TITLE REPERENCE: CLPR:244US
CURRENT APPLICATION NUMBER: US/11/066,648A
CURRENT FILING DATE: 2005-02-25
PRIOR FILING DATE: 2004-02-25
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VET. 2.1
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; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: BORISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: HOLM, Tom
; APPLICANT: APPLICANT: APPLICANT:
; APPLICANT: MATES, Stephen
; APPLICANT: MATIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; CURRENT APPLICATION HUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1044;
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CRGANISM: Bovine 19866880962402
US-10-750-185-58930
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13448 TATATATTTTATATATTTAAATTACATTTAAATTTTTATAATTTTAATTTTAATTTAAAT 43389
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                                                       TATATCATTGCCTAAGTTTTCTTATCAAGTTAAGTTTGGTGTCAACTACCCTCTAAATGT
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; Sequence 22, Application US/10829826B
; Publication No. US20050266397A1
; GENERAL INFORMATION:
; APPLICANT: BCKEr, David J.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Blyn, Lawrence B.
; APPLICANT: Hall, Thomas A.
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; APPLICANT: Hall,
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Publication No. US20050266397A1

GENERAL INFORMATION:

APPLICANT: Ecker, Dair, Steven A.

APPLICANT: Sampath, Rangarajan

APPLICANT: Blyn, Lawrence B.

APPLICANT: Hall, Thomas A.

APPLICANT: Hall, Thomas A.

TILLE OF INVENTION: WETHOD FOR IDENTIFICATION OF CORONAVIRUSES

FILE REFERENCE: IBISO075-100 (DIBIS-0058US)

CURRENT APPLICATION NUMBER: US/10/829,826B

CURRENT FILING DATE: 2004-04-22
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Pred. No. 4.3;
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 51.1<sup>1</sup>
Matches 97; Conservative
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: NIELSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR FILING DATE: 2006-05-04
NUMBER OF SEQ 1D NOS: 107
SOFTWARE: Patentin version 3.3
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                          Score 41.4; DB 6;
Pred. No. 1.6;
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43.4%; Pred. No. 6;
tive 0; Mismatches 246;
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Best Local Similarity 43.4%
Matches 189; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 31032
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                                                                                                     Length 31028;
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APPLICANT: Ecker, David J.
APPLICANT: Bampath, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Hall, Thomas A.
APPLICANT: Hall, Thomas A.
APPLICANT: Massire, Christian
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF CORONAVIRUSES
FILE REPERENCE: IBISO075-100 (DIBIS-0058US)
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                                                                                               Score 41.2; DE
Pred. No. 4.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.1%; Score 41.2; DE Best Local Similarity 51.1%; Pred. No. 4.3; Matches 97; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/829,8268
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEO ID NOS: 105
SOFTWARE: FABLESEO FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/10829826B Publication No. US20050266397A1 GENERAL INFORMATION:
                                                                                                 Query Match 5.1%;
Best Local Similarity 51.1%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10629 TGAAGATTTT 10638
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                                                                                                                                                                                                                                                                                                                                                                                                                                     471 TGACAAGTCT 480
                 ; TYPE: DNA; ORGANISM: Coronavirus US-10-829-8268-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Coronavirus
US-10-829-826B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 26
LENGTH: 31028
LENGTH: 31028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351
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RESULT 12 US-10-829-826B-23 ; Sequence 23, Application US/10829826B

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10449 TAGTACTGGTTGTCATACTGGTACTGATTTCAATGGGGATTTTTATGGTCCTTATAAGGA 10508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 TGGTATCATTGGATATTATGTTAATGACTTTAGGGTAGAATTTGAAGGTTCTTATGAGAA
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Publication No. US20050266397A1

GENERAL INFORMATION:
APPLICANT: Barbart, Rangarajan
APPLICANT: Sampath, Rangarajan
APPLICANT: Blyn, Lawrence B.
APPLICANT: Hall, Thomas A.
TITLE ON INVENTION: MESSITE, Christian
TITLE ON INVENTION: MESSITE, Christian
TITLE REPERENCE: IBIS0075-100 (DIBIS-0058US)
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 105

NUMBER OF SEQ ID NOS: 105

SOFTWARE: FastSEQ for Windows Version 4.0
                   GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Hofstadler, Steven A.
APPLICANT: Hally Lawrence B.
APPLICANT: Hall, Thomas A.
APPLICANT: Hall, Thomas A.
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF CORONAVIRUSES
FILE REFERENCE: IBIS0075-100 (DIBIS-0058US)
CURRENT PAPLICANT: 1004-04-22
NUMBER OF SEQ ID NOS: 105
SOUTHARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 51.1%; Pred. No. 4.3;
Matches 97; Conservative 0; Mismatches 93;
US20050266397A1
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ORGANISM: Coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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APPLICANT: OLEK, Alexander
APPLICANT: DLEK, Alexander
APPLICANT: DLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Gurt
ITLE OF INVENTION: Dy Assessing DNA Methylation
ITLE OF INVENTION: Dy Assessing DNA Methylation
ITLE OF INVENTION: Dy Assessing DNA Methylation
ITLE OF INVENTION: DY Assessing DNA Methylation
ITLE OF INVENTION: DY ASSESSING DNA METHYLATION
FILE OF INVENTION NUMBER: US/10/240,708
CURRENT APPLICATION NUMBER: DCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 100496-07
PRIOR APPLICATION NUMBER: DE 100496-07
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-10
PRIOR FILING DATE: 2000-09-01
SEQ ID NO 11
CONTROL DATE: 2000-09-01
CONTROL DATE: 2000-09-01
CONTROL DATE: 2000-09-01
CONTROL DATE: 2000-09-01
CONTROL DATE: 2000-09-01
CONTROL DATE: 2000-09-01
10569 GCTTTATGCTGCTATACTTAATAGTAATTGGTTTTGTACAAAGTGATAAGTGTTCTGT 10628
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                                                                                   411 GTCTCGAAATGCTACAAATAGTGATAATAAGTTTTATAGTACTAGAGAATAACGGCGTTGT
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4.9%; Score 40; DB 6; Length 6317;
Best Local Similarity 44.8%; Pred. No. 4.9;
Matches 154; Conservative 0; Mismatches 190; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 11, Application US/10240708; Publication No. US20050282157A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                 10629 İGAAGATİTİ 10638
                                                                                                                                                                                                TGACAAGTCT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGANATGCTACAAATAGTGATAATAAGTTTATAGTACTAGAGAATAACGGCGTTGTTGAC 474
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0
| Sequence 3947, Application US/10750185
| Sequence 3947, Application US/10750185
| Publication No. US200S0260603A1
| GENERAL INFORMATION:
| APPLICANT: MMI GENOMICS, INC.
| APPLICANT: RERR, Richard
| APPLICANT: ROSENFELD, David
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: BATES, Stephen
| APPLICANT: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| FILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
| CURRENT FILING DATE: 2003-12-31
| PRIOR APPLICATION NUMBER: US 60/437,482
| PRIOR FILING DATE: 2002-12-31
| PRIOR FILING DATE: 2002-12-31
| PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.8%; Score 39.2; DB 6; Length 12
48.6%; Pred. No. 4.6;
iive 0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 AAACCTTTTATTTACAACCTTAGTCATGATTATTAAAGTG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 AAGTCTCTTAATGTAAATGTTTGTTATGATATTGCTAGTG 514
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Job time : 842 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bovine 19866880742947
US-10-750-185-39647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIN version 3.1
SEQ ID NO 39647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.6*
Matches 107; Conservative
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Database: Published Applications NA Main:\*

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10: /cgn2\_6/ptodata/1/pubpna/USIO0\_PUBCOMB.seq:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

		Appl	Appl			Appl			Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	ID	US-09-811-007-45	US-10-062-624-45	US-10-062-051-45	US-10-062-920-45	US-10-680-349-45	US-10-731-554-45	US-10-059-964-23	US-10-314-639-23	US-10-901-714-23	US-10-901-774-23	US-10-059-964-25	US-10-314-639-25	US-10-901-714-25	US-10-901-774-25	US-09-811-007-41	US-10-062-624-41	US-10-062-051-41	US-10-062-920-41	US-10-680-349-41	US-10-731-554-41	US-10-059-964-47	US-10-314-639-47	US-10-901-714-47
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	Score	813	813	813	813	813	813	162.2	162.2	162.2	162.2	150.8	150.8	150.8	150.8	147.2	147.2	147.2	147.2	147.2	147.2	147.2	147.2	147.2
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Best Local Similarity 100.0%; Pred. No. 9.2e-181;
Matches 813; Conservative 0; Mismatches 0; Indels

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241 TTTACACGATCATATGACCCTACTTATGCAAGCAGTTTTGCAGGGTTTAGTGGTATCATT 300

05   61   GATGGTGTTTTTCTGAAGTTTTTCTGAAGGGAGGAGGAGCATTTATAGTAGTT   120   09   121   CAGTATAAAGTTGGTAATTTTTTTTTTTTTTTTTTTTTT	301 GGATATTATGTTAATGACTTTAGGGTAGATTTGAAGGTTCTTATGAGAATTTTGACCT  301 GGATATTATGTTAATGACTTTAGGGTAGAATTTGAAGGTTCTTATGAGAATTTTGACCT  301 GAAAAGAATTTTAATGACTTTAAGGGTAGAATTTTGAAGGTTCTTATGAGAATTTTTTTAGAATTTTTTTT		661 GGTTATTACCATAAGGTTGTAGGCATAGGCATGAGAGTAGAAATAGCTTACCATCCT	RESULT 3 US-10-062-051-45 Sequence 45, Application US/10062051 Sequence 45, Application US/10062051 Sequence 45, Application US/10062051 SENERAL INFORMATION: APPLICANT: Walker, David H. APPLICANT: Yu, Xue-Jie W. TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein TITLE OF INVENTION: Genes of Enrlichia canis and Uses Thereof FILE REFERENCE: D6152CIP2	; CURRENT FILING DATE: US/10/062,051 ; CURRENT FILING DATE: 2002-01-31 ; PRIOR APPLICATION NUMBER: US/09/660,587 ; PRIOR FILING DATE: 2000-09-12 ; PRIOR FILING DATE: 2092-03-03 ; NUMBER OF SEQ ID NOS: 46 ; SEQ ID NO 45 ; LENGTH: 813 ; TYPE: DNA ; ORGANISM: Ehrlichia canis
Db 241 TTTACACGATCATATGACCCTACTTATGCAAGCAGTTTTGCAGGGTTTAGTGTATCATT 300  Qy 301 GGATATTATGTTAATGACTTTAGGGTAGAATTTTGAAGGTTTTTGAAGTTTTTGAACCT 360	481 CTTAATGTAAATGTTTGTTATGTTAGTAGTGGTAGTATTCCTTTAGCACCTTATAG  481 CTTAATGTAAATGTTTGATATTGCTAGTGGTAGTATTCTTTTAGCACCTTATATG  541 TGTCCTGGTGCTGGTGCAGATTATATAAAGTTTTTAGGATATATCTTTTTTTT		0062624 Al us 28-Kilodalton f Ehrlichia canis	FILE REFERENCE: D61.5CIP2/D01. ; CURRENT PILING DATE: 2002-01-31 ; CURRENT FILING DATE: 2002-01-31 ; PRIOR PAPLICATION NUMBER: 09/660,587 ; PRIOR FILING DATE: 2000-09-12 ; NUMBER OF SEQ ID NOS: 46 ; SEQ ID NO 45 ; LENGTH: 813 ; TYPE: DNA ; PRATURE: ; FRATURE: ; OTHER INFORMATION: nucleic acid sequence of E. canis p28-9	Query Match         100.0%;         Score 813;         DB 5;         Length 813;           Best Local Similarity 100.0%;         Pred. No. 9.2e-181;         Added to the conservative of the conservative of the conservative of the conservative of the conservative of the conservative of the conservative of the conservation

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Best Local Similarity 100.0%; Pred. No. 9.2e-181;
Matches 813; Conservative 0; Mismatches 0;
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                                                                                                                     TYPE: DNA ORGANISM: Ehrlichia canis
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          E. canis p28-9
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Best Local Similarity 100.0%; Pred. No. 9.2e-181;
Matches 813; Conservative 0; Mismatches 0;
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; FEATURE:
; OTHER INFORMATION: nucleic acid sequence uS-10-062-051-45
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RESULT 4
US-10-062-920-45
IS-10-062-920-45

Sequence 45, Application US/10062920

Publication No. US20030096250A1

GENERAL INFORMATION:

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APPLICANT: Walker, David H. APPLICANT: McBride, Jere W. APPLICANT: Yu, Xue-Jie

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CURRENT APPLICATION NUMBER: US/10/062,920
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US/09/660,587
PRIOR FILING DATE: 1990-03-12
PRIOR FILING DATE: 1990-03-12
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NUMBER: OF SEQ ID NOS: 46
SEQ ID NO 45
LENGTH: 813 ö 601 199 721 721 661 8 8 ઠે g Š

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TATCAAGTTTAAGTTTGGTGTCAACTACCCTCTAAATGTTAATACTATGTTGTTTGGTGGG
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Publication No. US20040247616A1

GENERAL INFORMATION:

APPLICANT: Walker, David H.

APPLICANT: Walker, Jere W.

APPLICANT: Yu, Xue-Jiee W.

TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein

TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein

TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof

FILE REFERENCE: D6152CIP2

CURRENT APPLICATION NUMBER: US/10/731,554

CURRENT PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-09-12

NUMBER OF SEQ ID NOS: 46

SEQ ID NOS: 46
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Best Local Similarity 100.0%; Pred. No. 9.2e-181;
Matches 813; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Ehrlichia canis
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                                                                                                                Sequence 45, Application US/10680349
; Sequence 45, Application US/10680349
; Publication No. US20040198951A1
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: Wolstie, Jere W.
; APPLICANT: Wolstie, Jere W.
; APPLICANT: Wolstie, Jere W.
; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof; TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof; FILE REPERENCE: D615CIP2/D1
; CURRENT APPLICATION NUMBER: US/10/680,349
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CAGTATAAAGTTGGTATTCCCAATTTTAGTAATTTTTCAGCTGAAGAAACAATTCCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: nucleic acid sequence of E. canis p28-9 US-10-680-349-45
                     813
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                                      TTTGGTTGGGAGATTGGATTTAGATTTGCGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Ehrlichia canis
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                                                                                                                                   274 GTTACATTTCAAGATAATGCTGCTAGTTTCAGTGGAGCAATTGGATATTCTTACCCCGAA 333
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                                  TTAGGTCTTGATAAGTCT---GAGATAAATACTCACAGCAATTTTACACGATCATATGAC 258
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                                                              214 AAAAAAGİGCGICIİÇİAICGAICCIAACACITAIICAAACITICAAGGICCATATACI
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154 CATTTTAGCAATTTCTCAGTAAAGAAACTAATGTTGATACAATACAACTAGTAGGATAT
                                                                                                        259 CCTACTTATGCAAGCAGTTTTGCAGGGTTTAGTGGTATCATTGGATATTATGTTAATGAC
                                                                                                                                                                                 319 TTT---AGGGTAGAATTTGAAGGTTCTTATGAGAATTTTGAACCTGAAAGACAATGGTAC
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US-10-314-639-23
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Sequence 23, Application US/10059964

Publication No. US20020120115A1

GENERAL INFORMATION:
APPLICANT: Rikihisa, Yasuko
APPLICANT: Chasi, No. US20020120115A1io
TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia and Ehrlichia
TITLE OF INVENTION: Chaffeensis
FILE REFERENCE: 22727/04021
CURRENT PELING DATE: 2002-01-28
CURRENT PELING DATE: 2002-01-28
SARLIER PILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 33
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                                             GAAAGACAATGGTACCCTGAGAATAGCCAAAGCTACAATTTTTTTGCTTTGTCTCGAAAT
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Best Local Similarity 53.8%
Matches 432; Conservative
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; LOCATION: (1)..(840)
US-10-059-964-23
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                                                                                                                                                                                                                    Query Match 20.0%; Score 162.2; DB 8; Best Local Similarity 53.8%; Pred. No. 9.4e-28; Matches 432; Conservative 0; Mismatches 353;
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PRIOR APPLICATION UNMBER: 60/100,843
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 23
LENGTH: 840
                                                                                                                                         ; TYPE: DNA
; ORGANISM: Ehrlichia chaffeensis
US-10-901-714-23
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                                                                                         GTACTTGCATCTCTATTATCATTCTTATCTATTCAATCCTTTCAGCTATAAATCATAAT
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                      18;
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  Pred. No. 9.4e-28;
0; Mismatches 353;
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APPLICANT: OHASHI, NORIO
TITLE OF INVENTION: OUTER MEMBRANE PROTEIN (
TITLE OF INVENTION: CHAFFEENSIS
FILE REFERENCE: 22727-04109
CURRENT APPLICATION NUMBER: US/10/901,714
PRIOR APPLICATION NUMBER: 09/314,701
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594 TATCATAGAGTTATAGGGAATAAATTTTAAAAATTT---AAATGTTAACCATGTTGTTACA
                                    727 TIAICTGACGTTCCTAGAACTACTTCAGCTTCTGCTACTTTAAATACTGATTATTTTGGT
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18.5%; Score 150.8; DB 5; Length 8
Best Local Similarity 54.6%; Pred. No. 4.5e-25;
Matches 402; Conservative 0; Mismatches 307; Indels
                                                                                                      787 TGGGAGATTGGATTTAGATTTGC 809
                                                                                                                                       811 GGTGAAGCTGGAGTAAAGTTTAC 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (1)..(852)
US-10-059-964-25
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                                                                    APPLICANT: RIKHISA, YASUKO
APPLICANT: RIKHISA, YASUKO
APPLICANT: RIKHISA, YASUKO
APPLICANT: CHASHI, NORIO
TITLE OF INVENTION: CHAFFEENSIS
FILE REPERENCE: 22727-04109
CURRENT APPLICATION NUMBER: US/10/901,774
CURRENT PELLING DATE: 2094-07-29
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PATCHING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 69
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Pred. No. 9.4e-28;
0; Mismatches 353;
                     Sequence 23, Application US/10901774 Publication No. US20040265334A1 GENERAL INFORMATION:
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LENGTH: 840
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APPLICANT: RIKHISA, YASUKO

TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA

TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA

TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA

TITLE OF INVENTION: OUTER MEMBRANE PROTEIN OF EHRLICHIA CANIS AND EHRLICHIA

CURRENT APPLICATION NUMBER: 05/10/901,714

CURRENT PILING DATE: 1999-05-19

FRIOR APPLICATION NUMBER: 60/100,843

FRIOR APPLICATION NUMBER: 60/100,843

FRIOR APPLICATION NUMBER: 60/100,843

FRIOR APPLICATION OF SEQ ID NOS: 69

SOFTWARE: PATCHIN OF SEQ ID NOS: 69

SOFTWARE: PATCHIN OF SEQ ID NOS: 69
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  ----AATAAGTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCTCTTAATGTAAA
                                      471 AACAAATAAGTATGTTGTTATAAAGAACAATGGCTTATCTGTCGCATCCATTATAATCAA
                                                                            TGGTGCAGATTATATAAAGTTTTTAGGTATATCATTGCCTAAGTTTTCTTATCAAGTTAA
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pred. No. 4.5e-25;
0; Mismatches 307;
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APPLICANT: Rikihisa, Yasuko
APPLICANT: Ohasi, No. US20030103991Alio
TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia Canis and Ehrlichia
TITLE OF INVENTION: Chaffeensis
FILE REFERENCE: 22727/04021
CURRENT APPLICATION NUMBER: US/10/314,639
CURRENT FILING DATE: 2002-12-09
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
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TAAGGTTGTAGGTGATAGGCATGAGAGAGTAGAAATAGCTTACCATCCTACTGCATTATC 731
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                                                                                              GGTAGGTATCAGTTATCCATTATCTCTAATATGATTATATTTGCTGACGGATATTACCA
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                                                            GTTTGGTGTCAACTACCCTCTAAATGTTAATACTATGTTGTTTTGGTGGGGGTTATTACCA
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Pred. No. 4.5e-25;
0; Mismatches 307;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/10314639
Publication No. US20030103991A1
GENERAL INFORMATION:
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ORGANISM: Ehrlichia chaffeensis
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ilarity 54.6%;
Conservative
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Best Local Similarity
Matches 402; Conserv
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US-10-314-639-25
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NAME/KEY: CDS
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                              231 Grchattacagatataacaacaataaaaaartcaacattccrhataacacaaartrca 290
                                                                                                      291 AGATÁATGCTGTTAGCTTCAGTGCAGCTGTTGGATÁTATTTCCCAAGACAGTCCAAGGGT 350
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; Sequence 41, Application US/09811007
; Publication No. US2030185849A1
; GENERAL INFORMATION:
    APPLICANT: Walker, David H.
    APPLICANT: Walker, David H.
    APPLICANT: Walker, David H.
    APPLICANT: Walker, David H.
    APPLICANT: Walker, David H.
    APPLICANT: Wale-Jie
    TILE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
    TILE REPRENCE: D1522CTP
    TILE REPRENCE: D1522CTP
    CURRENT APPLICATION NUMBER: US/09/811,007
    CURRENT FILING DATE: 2001-03-16
    PRIOR PELLING DATE: 2000-09-12
    NUMBER OF SEQ ID NOS: 46
    SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                          471 AACAAATAAGTATGTTGTTATAAAGAACAATGGCTTATCTGTCGCATCCATTATAATCAA
                                                                                                                                                                                                                                                                                                                                                                                       GTTTGGTGTCAACTACCCTCTAAATGTTAATACTATGTTGTTTGGTGGGGGTTATTACCA
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11arity 53.2%; Pred. No. 3.1e-24;
Conservative 0; Mismatches 358;
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ORGANISM: Ehrlichia canis
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Best Local Similarity
Matches 445; Conserv
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Sequence 25, Application US/10901774

Sequence 25, Application US/10901774

GENERAL INFORMATION:

APPLICANT: RIKHISA, YASUKO

APPLICANT: OHASHI, NORIO

TITLE OF INVENTION: CHAFFEENSIS

FILE REFERENCE: 22727-04109

CURRENT APPLICATION NUMBER: US/10/901,774

CURRENT APPLICATION NUMBER: 09/14,701

PRIOR APPLICATION NUMBER: 60/100,843

PRIOR APPLICATION NUMBER: 60/100,843

PRIOR FILING DATE: 1998-05-19

NUMBER OF SEQ ID NOS: 69

SOOTWARE: Patentin Ver. 3.2

SEQ ID NO 25
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     AGAATTTGAAGGTTCTTATGAGAATTTTTGAACCTGAAAGACAATGGTACCCTGAGAATAG
                                                                                                             TGAAGCCTTCAGGTATATTGCTTTAGCAAGAGGAATTGATAATCTTCAAAAATATCCTGA
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Best Local Similarity 54.6%; Pred. No. 4.5e-25;
Matches 402; Conservative 0; Mismatches 307; Indels 27
                                                                           387 CCAAAGCTACAAATTTTTTGCTTTGTCTCGAAATGCTACAAATAGTGAT
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; ORGANISM: Ehrlichia chaffeensis
US-10-901-774-25
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ATGAATTACY           ATGAATTATY		ATAGGTAGTC       ATTAGTGCA	ATTCCTGGTA 		TTTGCAGGG	GGTTCTTATC		CTAGAGAAT!          CTTAAAAAT	AGTGGTAGT)    GCTGAAGGA(	TTTTAGGT2      ATTTTAAAG	CTAAATGTT7     ATCACACCAC	CATGAGAGAG       TTTGAGAAG	TCAGCTTCTC 
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